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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                       Sequence:
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Perfect score:
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PIR 79:*
1: pir1:*
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150
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                                                                                                                                                                                                                                                                283416 seqs, 96216763 residues
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                                                                                                                                                                                                                                                                                                                                                       QARQNLQNLFINFCLILICLLLICIIVMLL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                         7, 2005, 14:30:40 ; Search time 76 Seconds (without alignments) 37.980 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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probable cytochrom	protein-tyrosine k	protein kin-15 [im	large surface anti	large surface anti	large surface anti	hypothetical prote	hypothetical prote	hypothetical prote	common cytokine re	surface antigen -					

ALIGNMENTS

A;Status: translated from GB/EMBL/DDBJ A;Status: translated from GB/EMBL/DDBJ A;Residues: translated from GB/EMBL/DDBJ A;Residues: 1-52 <uy2> A;Residues: 1-52 <uy2> A;Cross-references: GB:M35393; NID:g164045; PIDN:AAC41618.1; PID:g164046 C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, ar C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplate; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation if C;Superfamily: cardiac phospholamban C;Superfamily: cardiac phospholamban C;Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; ti</uy2></uy2>	A; Molecule type: protein A; Residues: 1-35,'X',37-40,'X',42-45 <fu2> A; Residues: 1-35,'X',37-40,'X',42-45 <fu2> R; Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S. Nucleic Acids Symp. Ser. 17, 121-124, 1986 A; Title: Characterization of recombinant cDNA clones for canine cardiac phospholamban. A; Reference number: I46227; MUID:87174860; PMID:3562256 A; Accession: I46227; MUID:87174860; PMID:3562256</fu2></fu2>	A; Molecule type: protein A; Residues: 10-45 <sim> A; Residues: 10-45 <sim> A; Residues: 10-45 <sim> A; Residues: 10-45 <sim> A; Repidit, J:; Kadoma, M.; Tada, M.; Toda, H.; Sakiyama, F. R; Pujii, J:; Kadoma, M.; Tada, M.; Toda, H.; Sakiyama, F. Biochem. Biophys. Res. Commun. 138, 1044-1050, 1986 A; Title: Characterization of structural unit of phospholamban by amino acid sequencing fa, Reference number: A24818; MUID:86323152; PMID:3753485 A; Contents: partial sequence and acetylation site A; Accession: A24818</sim></sim></sim></sim>	A;Residues: 1-52 < UYE> A;Cross-references: GB:Y00399; NID:g911; PIDN:CAA68461.1; PID:g912 A;Cross-references: GB:Y00399; NID:g911; PIDN:CAA68461.1; PID:g912 R;Simmerman, H.K.B.; Collins, J.H.; Theibert, J.L.; Wegener, A.D.; Jones, L.R. J. Biol. Chem. 261, 13333-13341, 1986 J. Biol. Chem. 261, 13333-13341, 1986 A;Title: Sequence analysis of phospholamban. Identification of phosphorylation sites and A;Reference number: A25307; MUID:87008549; PMID:3759968 A;Contents: partial sequence and phosphorylation sites A;Accession: A25307	A;Residues: 1-52 <fuja: 1-52="" 15,="" 1987="" 6738,="" <fuja:="" a.;="" a26805;="" a26805<="" a;accession:="" a;cross-references:="" a;reference="" a;residues:="" a;title:="" acids="" canine="" cardiac="" cdna="" gb:m16012;="" in="" j.;="" k.;="" kadoma,="" kitano,="" m.;="" major="" mrna="" muid:87316936;="" nid:g164043;="" nucleic="" number:="" of="" phospholamban="" pid:g164044="" pidn:aaa30884.1;="" pmid:3628007="" pujii,="" r;uyeda,="" res.="" s.="" sequence="" tada,="" tanaka,="" td="" the="" uniprot:p61012;="" ventricular=""><td>RESULT 1 A29002 phospholamban - dog C;Species: Canis lupus familiaris (dog) C;Species: 23-Aug-1987 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004 C;Accession: A29002; A26805; A25307; A24818; I46227 R;Fujii, J.; Ueno, A.; Kitano, K.; Tanaka, S.; Kadoma, M.; Tada, M. J. Clin. Invest. 79, 301-304, 1987 A;Title: Complete complementary DNA-derived amino acid sequence of canine cardiac phosph A;Reference number: A29002; MUID:87083954; PMID:3793929 A;Accession: A29002</td><td>ALIGNMENTS</td></fuja:>	RESULT 1 A29002 phospholamban - dog C;Species: Canis lupus familiaris (dog) C;Species: 23-Aug-1987 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004 C;Accession: A29002; A26805; A25307; A24818; I46227 R;Fujii, J.; Ueno, A.; Kitano, K.; Tanaka, S.; Kadoma, M.; Tada, M. J. Clin. Invest. 79, 301-304, 1987 A;Title: Complete complementary DNA-derived amino acid sequence of canine cardiac phosph A;Reference number: A29002; MUID:87083954; PMID:3793929 A;Accession: A29002	ALIGNMENTS

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phospholamban
C;Species: Mus
C;Date: 19-Dec-
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A;Experimental source: cardiac muscle
A;Note: sequence extracted from NCBI backbone (NCBIN:116999, NCBIP:117001)
A;Note: sequence extracted from NCBI backbone (NCBIN:116999, NCBIP:117001)
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle sarcoplas
C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas
c; after phospholamban is the ca++ pump is activated and the rate of muscle relaxation is
C;Kopwords: acctylation, the Ca++ pump is activated and the rate of muscle relaxation is
C;Kopwords: acctylation end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
F;31-52/Domain: transmembrane #status predicted <TMM'>
F;1/Modified site: acctylated amino end (Met) #status predicted
F;16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predict
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R;Ganim, J.R.; Luo, W.; Ponniah, S.; Grupp, I.; Kim, H.W.; F. Circ. Res. 71, 1021-1030, 1992
A;Title: Mouse phospholamban gene expression during development of the control of the co
                                                                                                                                                                                      A;Cross-references: UNIPROT:P61015; GB:M63601; NID:g165636; R;Fujii, J.; Lytton, J.; Tada, M.; MacLennan, D.H. FEBS Lett. 227, 51-55, 1988
A;Title: Rabbit cardiac and slow-twitch muscle express the A;Reference number: S00249; MUID:88112222; PMID:2962883
A;Accession: S00249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phospholamban - rabbit
C;Species: Oryctolagus
C;Date: 28-Feb-1992 #se
C;Accession: B40424; SC
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F;1/Modified site: acetylated amino end (Met) #status experimental
F;1/Modified site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #s
           C; Comment:
                                                                             A; Molecule type: mRNA
A; Residues: 1-52 < FU2>
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G;Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_chan
C;Accession: B40424; S00249
R;Fujii, J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; Ma
J Biol. Chem. 266, 11669-11675, 1991
A;Tile: Structure of the rabbit phospholamban gene, cloning
A;Reference number: A40424; MUID:91268032; PMID:1828805
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A; Residues: 1-52 < FUJ>
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A;Accession: B40424
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Best L
                                          Cross-references:
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Dec-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
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Pred. No. 2.9e-11;
; Mismatches 0;
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                                                                                                                                                                                                                                                                       phospholamban
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               ai
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C;Species: Rattus norvegicus (Norway rat)
C;Species: O5-Mar-1994 #sequence_revision 27-Jun-1994 #text_
C;Aate: O5-Mar-1994 #sequence_revision 27-Jun-1994 #text_
C;Accession: S37638; I52270; I64795; I51840
R;Shanahan, C.M.; Weissberg, P.L.; Metcalfe, J.C.
Circ. Res. 73, 193-204, 1993
A;Title: Isolation of gene markers of differentiated and
A;Reference number: S37637; MUID:93284726; PMID:8508530
A;Accession: S37638
       R;Johns, D.C.; Feldman, A.M.
Biochem. Biophys. Res. Commun. 188, 927-933, 1992
A;Title: Identification of a highly conserved region at A;Reference number: I52270; MUID:93075183; PMID:1445334
A;Accession: I52270
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                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-52 < SHA>
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EMBL: X71068; NID: g313809;

PIDN:CAA50394.1;

PID: 93138

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proliferating vascular

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phospholamban - pig
C;Species: Sus scrc
C;Date: 21-Nov-1993
C;Accession: S05540
                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-52 <VER:
A; Cross-references: UNIPROT:P61013; EMBL:X15075; NID:92055; PIDN:CAA33171.1; PID:92056
A; Cross-references: UNIPROT:P61013; EMBL:X15075; NID:92055; PIDN:CAA33171.1; PID:92056
C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
C; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas,
e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation in
C; Superfamily: cardiac phospholamban
C; Superfamily: cardiac phospholamban
C; Superfamily: cardiac phospholamban
C; Reywords: acetylated amino end; AFPasse inhibitor; muscle; pentamer; phosphoprotein; tr
F; 31-52/Domain: transmembrane #status predicted <TMM'
F; 31-52/Domain: transmembrane #status predicted <TMM'
F; 16/Binding site: phosphate (Ser) (covalent) (by caMP-dependent kinase) #status predicte
F; 16/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p:
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A;Note: only one gene was detected A;Note: the single intron is upstream of the coding r C;Superfamily; cardiac phospholamban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: cDNA cloning and sequencing of phospholamban from A;Reference number: S05540; MUID:90056437; PMID:2530978 A;Accession: S05540
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C;Keywords: acetylated amino end; ATPase inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Verboomen, H.; Wuytack, Biochem. J. 262, 353-356,
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;Species: Sus scrofa domestica (domestic pig)
;Species: "\---1091 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
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                                                                                              Score 150; DB 1;
Pred. No. 2.9e-11;
; Mismatches 0;
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A;Molecule type: mRNA
A;Residues: 1-52 cHPA2>
A;Residues: 1-52 cHPA2>
A;Cross=references: GB:S95849; NID:g247934
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle sarcoplas
C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas
C;Comment: Phospholamban is the major phosphorylated and the rate of muscle relaxs
C;Comment: Phospholamban is the major phosphorylated and the rate of muscle relaxs
C;Superfamily: cardiac phospholamban
C;Keywords: acetylated amino end; ATPase inhibitor; cardiac muscle; heart; pentamer; pho
C;Keywords: acetylated amino end (Met) #status predicted
F;11-Modified site: acetylated amino end (Met) #status predicted
F;16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predict
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A; Residues: 1-52 <FUJ>
A; Residues: 1-52 = FUJ>
A; Crooss-references: UNIPROT: P26678; GB: M63603; NID: g189942; PIDN: AAA60083.1; PID: g189943
A; Crooment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, ar
C; Comment: Phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation;
e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation;
c; Comment: Helical transmembrane domains of five chains are thought to aggregate in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;FUjii, J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H. J. Biol. Chem. 266, 11659-11675, 1991
A;Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, A;Reference number: A40424; MUID:91268032; PMID:1828805
A;Accession: A40424
                                                                                                                                                                                                                                             A;Map position: 6q22.1-6q22.1
C;Superfamily: cardiac phospholamban
C;Superfamily: cardiac phospholamban
C;Keywords: accetylated amino end, ATPase inhibitor; muscle; pentamer; phosphoprotein;
F;31-52/Domain: transmembrane #status predicted <TMM>
F;31-52/Domain: transmembrane #status predicted <TMM>
F;16/Binding site: accetylated amino end (Met) #status predicted
F;16/Binding site: phosphate (Ser) (covalent) (by caNP-dependent kinase) #status prediffications are site; phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status
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C; Species: Homo sapiens (man)
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A;Cross-references: GDB:128300; OMIM:172405
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Adv. Exp. Med. Biol. 304, 387-395, 1991
A;Title: Cloning phospholamban cDNA from rat aortic smooth
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A;Residues: 1-52 <HWA1>
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A;Accession: I64795
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                                                                                                                                                          Query Match
Best Local
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Pred. No. 1.5e-10;
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Pred. No. 2.9e-11;
                                                                                                                         Mismatches
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A;Cross-references: GB:M59038
A;Note: the sequence of residues 3:
R;Toyofuku, T.; Zak, R.
submitted to GenBank, April 1991
A;Reference number: A44531
A;Accession: A44531
A;Molecule type: DNA
A;Residues: 1-52 (T03)
                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bentley, D.
submitted to the EMBL Data Library, June 1994
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C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, C; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcople; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation C; Genetics:

A; Note: only one gene was detected
A; Note: the single intron is upstream of the coding region
C; Superfamily: cardiac phospholamban
C; Superf
                                                                                                                                                                               A;Residues: 1-305 <BEN>
A;Cross-references: UNIPROT:Q20783; EMBL:U00067; PIDN:AAC77517.1; GSPDB:GN00021; CESP:F5
A;Experimental source: strain Bristol N2; clone F54E7
                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F54E7.5 - Caenorha C;Species: Caenorhabditis elegans C;Date: 29-Oct.1999 #sequence_revision C;Accession: T34299
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                                                                         A; Introns: 78/3; 173/3
                                                                                                             A; Map position:
                                                                                                                                              A; Gene: CESP:F54E7.5
                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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F;1/Modified site: acetylated amino end (Met) #status predicted
F;1/Kodified site: phosphate (Ser) (covalent) (by cAWP-dependent
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dep
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A;Molecule type: DNA
A;Residues: 1-52 <TO2>
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A;Title: Characterization of cDNA and genomic sequences A;Reference number: A39535; MUID:91170195; PMID:1825996 A;Accession: A39535
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C;Species: Gallus gallus (chicken)
C;Date: 06-Mar-1992 #sequence_revision
C;Datcession: A39535; B39535; A44531
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A; Residues: 1-17, 'L',
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Best Local Similarity
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T.; Zak,
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Pred. No. 9.
   Score
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   58
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(by calmodulin-dependent kinase) #s
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probable O-antigen/teichoic acid transporter CAC3065 [imported] - Clostridium
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: A81445
C;Accession: A81445
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVllet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyph; A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: A81445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein cotel - human (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 (;Accession: T08827
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A;Residues: 1-169 <PAR>
A;Coss-references: UNIPROT:Q9PIM9; GB:AL139074; GB:AL111168;
A;Experimental source: serotype O2, strain NCTC 11168
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C;Superfamily: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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;Cross-references: UNIPROT:P81408; EMBL:AF023268; NID:g2564910; PIDN:AAC51822.1;
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Introns: 75/3; 94/3; 131/3; 171/3; 207/3; 266/2; 299/3; 323/1;
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; Pred. No. 5.8;
4; Mismatches
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Pred. No. 27;
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3; Mismatches
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A,Cross-references: UNIPROT:P39209; EMBL:Z34005; NID:g496483; PIDN:CAA83970.1; PID:g4964 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

Nature 390, 249-256, 1997

NA; Wathors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, A,Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, A,Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteetlle, M.; Gawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteetlle, R.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Althors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Paresion. R69720; MUID:98044033; PMID:9384377

A. A. Casarion. R69720; MUID:98044033; PMID:9384377
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A;Cross-references: UNIPROT:097EP3; GB:AE001437; PIDN:AAK81005.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325, A;Accession: B97277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microbiology 140, 1847-1854, 1994
A;Title: Identification of TlpC, a novel 62 kDa MCP-like
A;Reference number: 140495; MUID:95005439; PMID:7921238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                  C; Superfamily: methyl-accepting chemotaxis protein
                                                                                                                                                                                                     A;Residues: Ĭ-215,'T',217-331,'P',333-573 <KUN>
A;Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12138.1; PID:g2632630
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                          A; Status: nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-573 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Hanlon, D.W.; Rosario, M.M.; Ordal, G.W.; Venema, G.; Van Sinderen, Microbiology 140, 1847-1854, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40496; B69724; S45067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methylation enzyme tlpC - Bacillus subtilis N; Alternate names: 62K MCP-like protein TlpC; methyl-accepting chemotaxis protein tlpC
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nonstructural protein 5B - human coronavirus (strain 229E)
(;Species: human coronavirus
(;Species: human coronavirus
(;Accession: C34038
C;Accession: C34038
R;Raabe, T.; Siddell, S.
Nucleic Acids Res. 17, 6387, 1989
A;Fitle: Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA 5 unique
A;Reference number: A34038; MUID:89366667; PMID:2701946
A;Rocession: C34038
A;Molecule type: genomic RNA
A;Residues: 1-77 RRAA>
A;Residues: 1-77 RRAA>
A;Residues: 1-77 RRAA>
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18531
R;Huang, Y:, Jellies, J:, Johansen, K.M.; Johansen, J.
J. Cell Biol. 138, 143-157, 1997
A;Title: Differential glycosylation of Tractin and LeechCAM, two novel Ig-superfamily A;Reference number: Z18951; MUID:97362067; PMID:9214388
A;Accession: T18531
                                                                                                                                                                                                               A;Title: Sequence analysis of human coronavirus 229E mRNAs 4 and 5: evidence for polymor A;Reference number: S25708; MUID:92230395; PMID:1373555
A;Accession: S25709
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 5 - human coronavirus

C;Species: human coronavirus 229E

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jul-2001

C;Dates S25709

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                                                                                                      A;Cross-references: EMBL:X64942; NID:g59462; PIDN:CAA46114.1; PID:g59464
C;Superfamily: coronavirus nonstructural protein 5B
                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-77 < JOU>
                                                                                                                                                                                                                                                                                                                           R;Jouvenne, P.; Mounir, S.; Stewart, J.N.; Richardson, C.D.; Talbot, P.J. Virus Res. 22, 125-141, 1992
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A;Molecule type: mRNA
A;Residues: 1-1880 <HUA>
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Query Match 35.0%;
Best Local Similarity 40.0%;
Matches 10; Conservative
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated

Please note that the curators of the UniProt database have purged some temporary accession

permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new accession number can be found by searching the old accession number in the UniProt Protein extension .rup) that can no longer be found in the database, the permanent record with the new If you encounter an accession number from an older search run against UniProt (results file accession number. Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

numbers members of the public who may encounter UniProt temporary accession include a copy of this attachment to assist any future Examiners or When submitting sequence search results for scanning into IFW, please Inis Page Blank (uspto)

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1: uniprot_sprot:*
2: uniprot_trembl:*
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P61014 mus musculu
P61013 sus scrofa
P61015 oryctolagus
P61016 rattus norv
P26679 homo sapien
P26677 gallus gall
Q81216 plasmodium
Q20783 caenorhabdi
Q9cqd6 mus musculu
Q6sle7 rattus norv
Q70794 cotesia kaz
Q9pim9 campylobact
Q6v267 bidessodes
Q8dxw1
Q8e310
000631
Q8r0c6
Q896t0
Q81je8
Q8hu78
Q6hu78
Q9br66
P81408
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Q80iw9
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P83556
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Q70v90
Q6ef12
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5 mycoplasma
6 rattus norv
6 plasmodium
0 cotesia voc
2 cotesia koe
1 streptococc
0 streptococc
1 homo sapien
6 mus musculu
0 clostridium
8 bacillus an
8 bacillus an
8 bacillus an
8 bacillus an
8 homo sapien
8 nomo sapien
7 xenopus lae
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squash leaf
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45	44	43	42	41	40	39	38	37	36	35	34	μ	32
53	53	53	53	53	53.5	53.5	53.5	54	54	54	54	54	54
35.3	35.3	35.3	35.3	35.3	35.7	35.7	35.7	36.0	36.0	36.0	36.0	36.0	36.0
263	263	245	245	113	217	217	130	720	513	482	434	434	433
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Q9WU52	Q925D4	Q7SME2	Q7SME1	Q8C8J2	Q6EF10	Q6EF08	Q70V97	Q40902	Q675R3	Q9MGA9	PIGU_RAT	PIGU_HUMAN	PIGU_MOUSE
Q9wu52 mue mueculu	Q925d4 rattus norv	Q7sme2 ovine enzoo	Q7smel ovine enzoo	Q8c8j2 mus musculu	Q6ef10 cotesia mel	Q6ef08 cotesia mel	Q70v97 cotesia fla	Q40902 petunia int	Q675r3 oikopleura	Q9mga9 chrysodidym	Q8chj1 rattus norv	Q9h490 homo sapien	Q8k358 mus musculu

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brimination."; J. Biol. Chem. 264:11468-11474(1989). -i- FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulumi- SUBUNIT: Homopentamer.	PHOSPHORYLATION SITES SER-16 AND THR-17. PHOSPHORYLATION SITES SER-16 AND THR-17. MEDLINE-89291905; PubMed=2544595; Megener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; Megener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; "Phospholamban phosphorylation in intact ventricles. Phosphorylation "Phospholamban phosphorylation in intact ventricles. Phosphorylation "Exercise 16 and threonine 17 in response to beta-adrenergic of serine 16 and threonine 17 in response to beta-adrenergic	SEQUENCE OF 10-45, AND PHOSPHORYLATION SITES SER-16 AND THR-17. MEDLINE=87008549; PubMed=3759968; MEDLINE=87008549; PubMed=3759968; Simmerman H.K.B., Collins J.H., Theibert J.L., Wegener A.D., Jones L.R.; "Sequence analysis of phospholamban. Identification of phosphorylation "Sequence analysis of phospholamban. Identification of phosphorylation sites and two major structural domains."; J. Biol. Chem. 261:13333-13341(1986).	[3] SEQUENCE OF 1-45, AND ACETYLATION. MEDLINE=86323152; PubMed=3753485; FUJii J. Kadoma M., Tada M., Toda H., Sakiyama F.; FUJii J. Kadoma M., Tada M., Toda H., Sakiyama F.; "Characterization of structural unit of phospholamban by amino acid sequencing and electrophoretic analysis."; sequencing and electrophoretic analysis."; Biochem. Biophys. Res. Commun. 138:1044-1050(1986).	ICI SEQUENCE FROM N.A. TISSUE=Heart ventricle; TISSUE=Heart ventricle; MEDLINE=87316936; PubMed=3628007; MY9eda A., Kitano K., Fujii J., Kadoma M., Tada M., Tanaka S.; "The cDNA sequence of the major phospholamban mRNA in canine cardiac ventricular muscle."; Ventricular muscle."; Nucleic Acids Res. 15:6738-6738(1987).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=87083954; PubMed=3793929; Fujii J., Ueno A., Kitano K., Tanaka S., Kadoma M., Tada M.; "Complete complementary DNA-derived amino acid sequence of canine cardiac phospholamban."; Cardiac phospholamban.";	NamosPLN; Canis familiaris (Dog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. NCBI_TaxID=9615;	CANPA PPLA CANFA STANDARD; PRT; 52 AA. P61012; P07473; P1-APR-1988 (Rel. 07, Created) 01-APR-1988 (Rel. 07, Last sequence update) 25-CCT-2004 (Rel. 45, Last annotation update) Cardiac phospholamban (PLB).

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25-OCT-2004 (Rel. 45, L
Cardiac phospholamban (
              SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Aorta, Heart, and Kidney;

MEDLINE=2235468; PubMed=12466851; DOI=10.1038/nature01266;

Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Okazaki Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

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Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
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MOD_RES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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      Gaasterland T.,
Grimmond S., Gu
                                                                                                                                                                                                                                                                                    vitro
                                                                                                                                                                                                                                                                                                MEDLINE=93008802; PubMed=1394867;
Ganim J.R., Luo W., Ponniah S., Grupp I., Kim H.W., Ferguson D.G.,
Kadambi V., Neumann J.C., Doetschman T., Kranias E.G.;
"Mouse phospholamban gene expression during development in vivo and
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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PIRSF; PIRSF001665; PIB; 1.
TICRPAMs; TIGR01294; P lamban; 1.
Acetylation; Direct protein seque
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Phosphothreonine (by CaMK1).
076361D9ADC424D3 CRC64;
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TIGRFAMs; TIGR01294; P lamban; 1.
Acetylation; Phosphorylation; Transmembrane.
Acetylation; Phosphorylation; Cytoplasmic (Potential).
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MGD; MGI:97622; Pln.
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; P07473; 1FJK.
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RX MEDLINE-2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Detow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robask S.A., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon B., Ketteman M., Madan A., Godrigues S., Sanchez A.,
RA Hhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Bothesrield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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RA Magalott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wilming L.G., Wynshaw-Boris A., Zaimmer A., Carninci P., Hayatsu N.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Azakawa T., Fukuda S.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Azakawa T., Fukuda S.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Mirney E., Hayashizaki Y.,
RA Mirney E., Hayashizaki Y., Materston R., Lander E.S., Rogers J.,
RA Miyasis of the mouse transcriptome based on functional annotation of
EMBL; $46792; AAB23706.1; --
EMBL; AK002622; BAB22237.1; --
EMBL; AK007118; BAG30680.1; --
EMBL; AK052199; BAG34880.1; --
EMBL; BC061097; AAH61097.1; --
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modified and this statement is not removed. Usage by a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the phospholamban family.
                                                                                                                                                                                                                        ss requires a license agreement (See http://www.isb-sib.ch/announce/lan email to license@isb-sib.ch).
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Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lamberth S., Griesinger C., Schmid H., Cararoll B., Vorherr T., Krebs J.;

"NMR solution structure of phospholamban membrane p submitted (AUG-2000) to the PDB data bank.

-I- FUNCTION: phospholamban has been postulated to provide the provided that the the provid
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Cardiac phospholamban (PLB).
                                                                                                                                                                                                           PDB; 1FJK; NMR;
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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TISSUE=Smooth muscle;
MEDLINE=90056437; PubMed=2530978;
MUVtack F., Eggermont J.A.,
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TISSUE=Smooth
                                                                                                                                                                                                                                                        EMBL; X15075; CAA33171.1;
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                                                                                                                                               CIGRFAM8;
                                                                                                                           D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity of the calcium pump of cardiac sarcoplasmic SUBUNIT: Homopentamer (By similarity). SUBCELLULAR LOCATION: Membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the phospholamban family.
               rero; IPR005984; p lamban.
7; PIRSP001665; pt.ll; 1.
7AM5; TIGR01294; p lamban; 1.
ructure; Acetylation; Phospho
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               N-acetylmethionine (By similarity). Phosphoserine (by PKA) (By similarity). Phosphothreonine (by CaMK1) (By
similarity).
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.2e-10;
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                  Intact; p61015; ...

Interpro; IRR005994; P lamban.

PIRSF; PIRSF001665; PLB; 1.

TIGRFAMs; TIGR01294; P lamban; 1

Acetylation; Phosphorylation; Transmem 1 1 31 Pott TRANSMEM 32 52 Pott MOD_RES 16 16 Phosphorylation; Transmem 1 1 N-ax MOD_RES 17 17 Phosphorylation; Prosphorylation; Transmem 1 1 Pott Transmem 1 1 Pott Transmem 1 1 Pott MOD_RES 16 16 Phosphorylation; Prosphorylation; Prosphoryla
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TURN
SEQUENCE
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EMBL; M63601; AAA31445.1; -.
EMBL; Y00761; CAA66730.1; -.
PIR; B40424; B40424.
                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDITUR=9128032; PubMed=1828805;

Fujii J., Zarain-Herzberg A., Willard H.F., Tada M.,

"Structure of the rabbit phospholamban gene, cloning
cDNA, and assignment of the gene to human chromosome
J. Biol. Chem. 266:11669-11675(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLA RABIT STANDARD;
P61015; P20006;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
25-OCT-2004 (Rel. 45, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88112222; PubMed=2962883; DOI=10.1016/0014-5793(88)81412-1; Fujii J., Lytton J., Tada M., Maclennan D.H.; "Rabbit cardiac and slow-twitch muscle express the same phospholambi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                    HSSP; P07473; 1FJK.
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SUBCELLULAR LOCATION: Membrane.
TISSUE SPECIFICITY: Heart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Phospholamban activity of the calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EW
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Phosphoserine (by PKA) (By similar
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                                                                               Transmembrane.
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Pred. No. 1.2e-10;
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                                                                       EMBL; L03382; AAA41849.1; -.
EMBL; X71068; CAA50394.1; -.
EMBL; S95849; AAN86727.1; -.
EMBL; S95853; AAB21903.1; -.
PIR; S37638; S37638.
HSSP; P07473; 1FJK.
                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                      Shanahan C.M., Weissberg P.L., Metcalfe J.C.; "Isolation of gene markers of differentiated and proliferating vascular smooth muscle cells.";
InterPro; IPR005984; Plamban.
PIRSF; PIRSF001665; PIB; 1.
TIGRFAMS; TIGR01294; P lamban; 1.
Acetylation; Phosphorylation; Transmembrane DOMAIN
1 31 Cytoplasmic (PTRANSMEM 32 52 Potential.
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92206263; PubMed=1725098; Hwang K.S., Nadal-Ginard B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Aortic
                                                                                                                                                                                                                                                                                                                                                                                                                                  Circ. Res. 73:193-204(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93284726; PubMed=8508530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johns D.C., Feldman A.M.; "Identification of a highly conserved region at the phospholamban gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93075183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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Pred. No. 1.2e-10;
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RESULT 6
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                                                                                                  WEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
X Hopkins R.F., Jordan H., Moore T., Max, Rubin G.M., Hong L.,
X Hopkins R.F., Jordan H., Moore T., Max, Rubin G.M., Hong L.,
X Hopkins R.F., Jordan H., Moore T., Max, Rubin G.M., Prange C.,
X Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Stapleton M., J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
X Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
X Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,
X Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
X Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
X Hollaho D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
X Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
X Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
X Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
X Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
X Chang A. C., Schein J. F., Tones S. I., Mastra M. A.,
X Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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25-OCT-2004
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MOD_RES
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                  Proc.
                                                     Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,00 and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of human cardiac phospholamban."; Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salvatore C.A., Jacobson M.A.; "Cloning of human cardiac phos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujii J., Zarain-Herzberg A., Willard H.F., "Structure of the rabbit phospholamban gene, cDNA, and assignment of the gene to human ci J. Biol. Chem. 266:11669-11675(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McTiernan C.F., Frye C.S., Lemster B.H., Kinder E
Ogletree-Hughes M.L., Moravec C.S., Feldman A.M.;
"The human phospholamban gene: structure and expr
J. Mol. Cell. Cardiol. 31:679-692(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99222499; PubMed=10198197; DOI=10.1006/jmcc.1998.0904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Phosphoserine (by PKA) (By similar:
Phosphothreonine (by CaMK) (By
similarity).
0763601F76AB54D3 CRC64;
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Pred. No. 1.2e-10;
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Query Match
Best Local Similarity
Matches 29; Conser
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EMBL; M60411; AAA60109.1; -.
EMBL; M60411; AAD55595.1; -.
EMBL; BC005269; AAH05269.1; -.
EMBL; BC005269; AAH05269.1; -.
PIR; A40424; A40424.
PDB; 1K9N; Model; A/B/C/D/E=35-52.
PDB; 1K9N; Model; A/B/C/D/E=35-52.
PDB; 1FLN; Model; A/B/C/D/E=35-52.
PDB; 1PLN; Model; A/B/C/D/E=35-52.
PDB; 1PLN; Model; A/B/C/D/E=1-52.
Genew; HONC:9080; PLN.
Genew; HONC:9080; PLN.
                                                                                                                                                                                                                                                                                              InterPro; IPR005984; P lamban.
Pfam; PF04272; Phospholamban; 1.
PfRSF; PIRSF001665; PLB; 1.
TIGRFAMS; TIGR01294; P lamban; 1.
3D-structure; Acetylation; Phosphor; DOWALIN
1 31 Cytopli
TRANSMEM 32 52 Potent;
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"Using experimental information to produce a model of the
transmembrane domain of the ion channel phospholamban.";
Biophys. J. 74:1203-1214(1998).

-I. FUNCTION: Phospholamban has been postulated to regulate the
activity of the calcium pump of cardiac sarcoplasmic reticul
-I. SUBCELLULAR LOCATION: Membrane.
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"Solution structure of the cytoplasmic domain of phospholamban: phosphorylation leads to a local perturbation in secondary
                                                                                                                                                                                                                                     XITAH
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structure.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98170970; PubMed=9512019;
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                                                                                        0
                                                                                        Score 144; DB 1;
Pred. No. 6.3e-10;
D; Mismatches 1
                                                                                                                                                                                                                                                                               N-acetylmethionine (By similarity). Phosphoserine (by PKA) (By similarity). Phosphothreonine (by CaMK) (By similarity).
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EMBL; M59037; -; NOT ANNOTATED CDS
EMBL; M59038; AAA63167.1; -.
PIR; A39535; A39535.
HSSP; P07473; 1FJK.
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01-AUG-1992 (Rel. 23, Last sequence up
25-0CT-2004 (Rel. 45, Last annotation
Cardiac phospholamban (PLB).
                                                                                                                                                                                                                                                                                                                         InterPro; IPR005984; P lamban.
Pfam; PF04272; Phospholamban; 1.
PIRSF; PIRSF001665; PLB; 1.
TIGRFAMs; TIGR01294; P lamban; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- PTM: Phosphorylated in response to beta-adrenerg-i- SIMILARITY: Belongs to the phospholamban family.
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-!- SUBCELLULAR LOCATION: Membrane.
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activity of the calcium pump of cardiac sarc
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MEDLINE=91170195; PubMed=1825996;
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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WHALL N. Pain A., Berriman M., Churcher C., Harris B., Harris D.,

WA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,

WA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,

Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,

Chillingworth T., Christodoulou Z., Clark L., Clark R., Doggett J.,

Cronin A., Davies R., Davis P., Dear P., Dearden P., Doggett J.,

Pathwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,

Hamphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,

WA Knights A., Konfortov B., Kyes S., Larke N., Lawpon D., Lennard N.,

WA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,

Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,

WA Rajandream M.A., Rutter S., Smith R., Squares R., Squares S., Stevens K.,

Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,

Na Seeger K., Tivey A., Unwin L., Whitehead S., Woodward J.,

Wature 419:527-531(2002).
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F54E7.5.
Name=F54E7.5; ORFNames=F54E7.5;
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Eukaryota; Alveolata;
STRAIN=Bristol
                                       SEQUENCE FROM
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Submitted
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                                                                                                                                                                                                                                                                                                                                                                                     Bentley D.;
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WormBase Consortium,
"Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
MEDLINE=99069613;
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                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                     (OCT-1994)
                                                                                                                   (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aı protein.
792 AA; 9
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                                       N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9851916;
                                                                                                                                                                                                                                                                                                     . elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.7%;
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                                                                                                                                                                                                                                                                                                         cosmid F54E7.";
EMBL/GenBank/DDBJ databases.
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                                                                                                                   EMBL/GenBank/DDBJ
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Pred. No. 5
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RESULT 10
SARL MOUSE
ID SARL N
                      RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Anikaido I., Osato N., Saito R., Suzuki H., Schonbach C., Gojobori T.,
RA Aggi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Kangin A., Watsuda H., Batalov S., Belsel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Gaasterland T., Gartinoldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Hinozancki Filmshiran T. Konnu H. Nabamura M. Saro K.
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Matches
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TISSUE-Manmary gland;
TISSUE-Manmary gland;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.
Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003
28-FEB-2003
05-JUL-2004
                                                                                                                                                                                                           Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotati 60,770 full-length cDNAs ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2004) to the EMBL; U00067; AAK20074.1; PIR; T34299; T34299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WormBase; WBGene00018828; F54E7. WormBep; F54E7.5; CE01316. Hypothetical protein. SEQUENCE 305 AA; 34300 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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41,
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Last annotation updat
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Pred. No. 3;
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                                                                                                                                                                                                                                                              functional annotation
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RESULT 11
Q6SLE7
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Best Local S
Matches 11
STRAIN=Wistar; TISSUE=Atrium;
Minamisawa S., Yokoyama U., Sato Y.,
Mori H., Ishikawa Y.;
Submitted (NOV-2003) to the EMBL/GenE
EMBL; AY456000; AAR19044.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0030234; F:enzyme regulator ac
InterPro; IPR008028; Sarcolipin.
Pfam; PF05366; Sarcolipin; 1.
SEQUENCE 31 AA; 3808 MW; 9B310161
                                                                                                                                                                                                                                                                                                                                                           Q6SLE7;
Q6SLE7;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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EMBL; AK008896; BABZ5959.1; -.
EMBL; AK009005; BABZ6019.1; -.
EMBL; AK009809; BABZ6516.1; -.
EMBL; BC028496; AAHZ8496.1; -.
HSSP; 000631; 1JDM.
                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sarcoplasmic TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murny D.M., Sodergren B.J., Lu X., Glbbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and course of the second state o
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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PF05366; Sarcolipin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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8 25 Potential
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                      Sato Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 6.3,
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58;
Pred. No.
    9B310161575EF81D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9B310161575EF81D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential
                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                               activity;
                                                                                                                                                                   Nakagome
                                                                                                                                                                                                                                                                                                                                                                                                                                                31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ₿
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                                                                 IEA.
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                                                                                                                              databases
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                                                                                                                                                                      Mouri M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT 12
Q70V94
ID Q70V9
AC Q70V9
AC Q70V9
DT 05-JU
DT 0
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Q9PIM9
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L Syst Entomol. 29:371-382(2004).

C -[- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

C -[- SIMILARITY: Belongs to the complex I subunit 1 family.

R EMBL, AJ535966; CAD59806.1; -.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0005739; C:mitochondrion; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0006118; P:electron transport; IEA.

R InterPro; IPR001694; Resp_NADH_dh1.

R InterPro; IPR001694; Resp_NADH_dh1.

Pfam; PF00146; NAD; Oxidoreductase; Transmembrane; Ubiquinone.

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T NON_TER 130 130
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                     Q9PIM9 PRELIMINARY; PRT; 1
Q9PIM9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 25, Last seque:
01-MAR-2004 (TrEMBLrel. 26, Last annot.
Putative integral membrane protein.
OrderedLocusNames-Cj0266.3, Cj0266c;
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=NCTC 11168;
MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
MEDLINE=20150912; Mungall K.L., Ketley J.M., Churcher Parkhill J., Wren B.W., Mungall K.L., Feltwell T., Holro Basham D., Chillingworth T., Davies R.M., Feltwell T., Holro
                                                                                                                                                                Campylobacterae; Epsilonproteobacteria; Campylobacterales;
NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Preliminary evolutionary relationships genus Cotesia (Hymenoptera: Braconidae: analysis of four molecular markers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q70V94
Q70V94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea;
Braconidae; Microgastrinae; Cotesia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TremBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=NADH1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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130 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whitfield J.B.;
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Lrel. 27, Last annotation update)
subunit 1 (Fragment).
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45.8%;
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Last annotation update)
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Pred. No.
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Pred. No. 22;
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family.
                                     Holroyd
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Best Local :
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Best Local
                                    Q8BS41 PRELIMINARY; PRT;
Q8BS41;
Q8BS41;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence of the sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Evolution of subterranean diving beetles (Coleoptera: I Hydroporini, Bidessini) in the arid zone of Australia."; Evolution 57:2819-2834(2003).

-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubi.
-!- SIMILARITY: Belongs to the complex I subunit 1 famil: EMBL; AY353827; AAR02201.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
InterPro; IPR001694; Resp_NADH_dh1.
Pfam; PF00146; NADHdh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6V2B7 PRELIMINARY; PRT; 35 AA.
Q6V2B7;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1 (Fragment).
Bidessodes limestonensis.
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PIR; A81445; A81445.
InterPro; IPR010916; TONB Box N.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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PubMed=14761060;
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Neoptera; Endopterygota; Coleoptera; Adephaga; Dytiscidae;
Hydroporinae; Bidessini; Bidessodes.
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                            insert sequence
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genome sequence of the food-borne pathogen Campylobacter jejuni
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169 AA; 19512 MW;
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ta and vein cDNA, RIKEN full-length
0008A08 product:hypothetical proteil
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RE STRAIN-C57BL/61; TISSUE-AORTA and vein;

RA Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Adachi J., Alzawa K., Hanagaki T., Hara A., Hashizume W.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume T.,

RA Hayashida K., Hayatsu N., Hiraoka T., Hiraoka T., Hiraoka T., Itoh M., Kagawa I., Kasukawa T.,

RA Hori F., Imotani K., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saltoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/6J; TISSUE=Aorta and vein;
STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=20499374, PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374, PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It.
Konno H., Okazaki Y., Muramatsu M., Hayashiraki Y.;
Whormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new ge Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahika M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Muramatsu S., Kawai J., Panaka T., Ozawa K., Tanaka T., Hayashizaki Y.; Muramatsu S., Kawai J., Wataning pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Nature 409:685-690(2001)
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STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
[1]
                                                                                                                                     Hypothetical protein. SEQUENCE 110 AA; 1
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Meth. Enzymol. 303:19-44(1999)
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                                                                                                                                                                                                       EMBL; AK040657; BAC30658.1;
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nilarity 42.9%;
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                                   Score 56;
Pred. No.
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Sciurognathi; Muridae; Murinae; Mus
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US-09-193-104-16	US-09-193-104-15	US-09-193-104-14	US-09-193-104-13	US-09-134-000C-4489	US-09-693-746-22	US-09-270-767-48513	US-09-270-767-33296	US-09-270-767-55014	US-09-270-767-39797	US-09-060-939A-2	US-09-909-280A-2	US-09-293-505-2	US-09-207-857-2	US-09-060-939A-7	US-09-293-505-7	US-09-107-532A-4559	US-09-500-063-2
Sequence 16, Appl	Sequence 15, Appl	Sequence 14, Appl	Sequence 13, Appl	Sequence 4489, Ap	Sequence 22, Appl	Sequence 48513, A	Sequence 33296, A	Sequence 55014, A	Sequence 39797, A	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 4559, Ap	Sequence 2, Appli

ALIGNMENTS

RESULT 1 US-09-252-063-3

Sequence 3, Application US/09252063 Patent No. 6538022

GENERAL INFORMATION:

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APPLICANT: Ovaska, Martti
APPLICANT: Ovaska, Martti
APPLICANT: Ovaska, Martti
APPLICANT: Vidgren, Jukka
APPLICANT: Yilpertula-Ikonen, Marjo
APPLICANT: Yilpertula-Ikonen, Marjo
APPLICANT: Yilpertula-Ikonen, Marjo
APPLICANT: Tilgmann, Carola
APPLICANT: Lotta, Timo
APPLICANT: Carola
APPLICANTION: Ca-Arpase (Phospholamban Inhibitors)
FILE OF INVENTION: Ca-Arpase (Phospholamban Inhibitors)
FILE REFERRICE: 1102.0250001
FILE REFERRICE: 1102.0250001
FILE REFERRICE: 1102.0250001
FILE REFERRICE: 1102.0250001
FILER APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1997-09-18
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER APPLICATION STEP 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 52
TYPE: PRT
ORGANISM: Canis sp.
TISCAN-3-5-2-063-3
Sequence 4, Application US/09252063
Patent No. 6538022
GENERAL INFORMATION:
APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vijperttula-Ikonen, Marjo
APPLICANT: Tilgmann, Carola
APPLICANT: Lotta, Timo
APPLICANT: Kaivola, Juha
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US-09-252-063-4
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Matches
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                                                                            Marjo
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APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Ylipertula-Ikonen, Marjo
APPLICANT: Ylipertula-Ikonen, Marjo
APPLICANT: Tilgmann, Carola
APPLICANT: Lotta, Juha
APPLICANT: Lotta, Juha
APPLICANT: Lotta, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.025001
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER APPLICATION SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
SEQ ID NO 5
SEQ ID NO 5
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CURRENT APPLICATION NUMBER: US/09/252,063

CURRENT FILING DATE: 1999-02-18

EARLIER APPLICATION NUMBER: 08/937,117

EARLIER FILING DATE: 1997-09-24

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 52

TYPE: PRT

ORGANISM: Oryctolagus cuniculus
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                                                                                                                              GENERAL INFORMATION:
                                                                                                                                               Sequence 6, Application US/09252063 Patent No. 6538022
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APPLICANT: Pollegello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Tenhunen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Yliperttula-Ikonen, Marjo
APPLICANT: Tilgmann, Carola
APPLICANT: Lotta, Timo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 52
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No. 653802
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ilarity 100.0%;
Conservative 0
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Pred. No. 4.4e-13;
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Pred. No. 4.4e-13;
; Mismatches 0;
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     PRIOR APPLICATION NUMBER: GB 9908670.4
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APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
FULE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION UNMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
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; ORGANISM: Mus
US-09-252-063-6
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US-09-549-872B-14
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NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 52
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                                                                                                                                                        Sequence 15, Application US/09549872B Patent No. 6540996
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APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Broenen, Jose
APPLICANT: Bogeert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (GRV/RE)
CURRENT APPLICATION UNMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: Compounds for Deactiv:
TITLE OF INVENTION: Co-ATPase (Phospholami
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: U9/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 08/937,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Sus
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llarity 100.0%;
Conservative 0
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Pred. No. 4.4e-13;
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Pred. No. 4.4e-13;
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; ORGANISM: Homo sapiens
US-09-549-872B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function (
TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.025001
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US/09/722,440
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/252,063
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 10
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 52
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PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
LENGTH: 52
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Best Local Similarity
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APPLICANT:
APPLICANT:
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Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0;
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APPLICANT: Yliperttula-Ikonen, Marjo
                                                                                        APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Marti
APPLICANT: Tenhunen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
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                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Canis sp.
CANT: Tilgmann, Carola
CANT: Lotta, Timo
CANT: Kaivola, Juha
COP INVENTION: Compounds for Deactivating Phospholamban Function on
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Vidgren, Jukka
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RESULT 10 US-09-722-440-6

GENERAL INFORMATION:

APPLICANT: Pollesello, Piero APPLICANT: Ovaska, Martti

APPLICANT: APPLICANT: APPLICANT:

Tenhunen, Jukka Vidgren, Jukka Vilgertnula-Ikonen, Marjo Vilgeann, Carola Lotta, Timo

APPLICANT:

PPLICANT:

Kaivola, Juha

Sequence 6, Application US/09722440 Patent No. 6774103

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APPLICANT: Ovaska, Martti
APPLICANT: Tenhunen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vilgerttula-Ikonen, Ma
APPLICANT: Tilgmann, Carola
APPLICANT: Lotta, Timo
                                                                                                                                                              SEQ ID NO 5
LENGTH: 52
TYPE: PRT
ORGANISM: Rattus sp.
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                                                                                                           Query Match
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Best Local :
                                                                                                                                                                                                                                                                                                    APPLICANT: Lotte, Timo
APPLICANT: Kaivola, Juha
APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban
TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/722,440
CURRENT FILING.DATE: 2000-11-28
CURRENT FILING.DATE: 2000-11-28
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CURRENT FILING DATE: 2000-11-28
ERIOR APPLICATION NUMBER: 09/252,063
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/252,063
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Ca-ATPA FILE REFERENCE: 1102.0250001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Oryctolagus cuniculus
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                                                                                          Similarity
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                                                                         Conservative
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                                                                                        100.0%; Score 150; DB 4; 100.0%; Pred. No. 4.4e-13;
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APPLICANT: Ovaska, Martti
APPLICANT: Ovaska, Martti
APPLICANT: Ovaska, Martti
APPLICANT: Vidgren, Jukka
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Kaivola, Juha
ITILE OF INVENTION: Compounds for Deactivating Phospholamban Function on
ITILE OF INVENTION: Ca-ATPBase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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; LENGTH: 52
; TYPE: PRT
; ORGANISM: MUS E
US-09-722-440-6
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US-09-252-063-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-252-063-1
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GENERAL INFORMATION:

APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Tenhunen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Yligerttula-Ikonen, Marjo
APPLICANT: Tilgmann, Carola
                                                                                                                                            Sequence 2, Application US/09252063 Patent No. 6538022
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FILE REFERENCE: 1102.0250001

CURRENT APPLICATION NUMBER: US/09/722,440

CURRENT FILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-21-8

PRIOR FILING DATE: 1999-02-18

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0
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96.7%;
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Pred. No. 2.7e-12;
0; Mismatches 1
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APPLICANT:

Tenhunen, Jukka Vidgren, Jukka Yliperttula-Ikonen, Marjo

APPLICANT:

Tilgmann, Carola

APPLICANT: Pollesello, Pie APPLICANT: Ovaska, Martti APPLICANT: Tenhunen, Jukk

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                                                    RESULT 14
US-09-722-440-2
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US-09-722-440-1
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; ORGANISM: Sus
US-09-252-063-2
Sequence 2, Applicat Patent No. 6774103 GENERAL INFORMATION:
                                                                                                                                                                                             Query Match 96.0%;
Best Local Similarity 96.7%;
Matches 29; Conservative
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LENGTH: 52
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LENGTH: 52
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
TITLE OF INVENTION: CA-TPBASE (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/722,440
CURRENT FILING DATE: 2000.11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Tenhunen, Jukka
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TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
TITLE OF INVENTION: Ca-ATPage (Phospholamban Inhibitors)
FILE REFERENCE: 1102.025001
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTMARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/252,063
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                1 QARQNLQNLFINFCLILICLLLICIIVMLL 30
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                                  Application US/09722440
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Vidgren, Jukka
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Tilgmann, Carola
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96.7%;
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Pred. No. 2.7e-12;
                                                                                                                                                                                                                Score 144; DB 4; Length 52; Pred. No. 2.7e-12;
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; APPLICANT: KAIVOIA, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; TITLE OF INVENTION: Compounds (Phospholamban Inhibitors)
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/722,440
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/252,063
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus sp.
Search completed: July 7, 2005, 15:44:07 Job time : 91 Becs
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US-09-949-016-7310
; Sequence 7310, Application US/09949016
; Patent No. 6812339
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-109-08
PRIOR PILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7310
SEQ ID NO 7310
TYPE: PRT
ORGANISM: Human
3-09-949-016-7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 96.0%; Score 144; DB 4; Length 52; Best Local Similarity 96.7%; Pred. No. 2.7e-12; Matches 29; Conservative 0; Mismatches 1; Indels
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Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                                           Lotta, Timo
                                                                                                                                                                                    96.0%; Score 144; DB 4; Length 89; llarity 96.7%; Pred. No. 4.8e-12; Conservative 0; Mismatches 1; Indels
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Result
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/02

2: /cgn2 6/ptodata/1/pubpaa/03

3: /cgn2 6/ptodata/1/pubpaa/03

4: /cgn2 6/ptodata/1/pubpaa/04

4: /cgn2 6/ptodata/1/pubpaa/04

5: /cgn2 6/ptodata/1/pubpaa/04

6: /cgn2 6/ptodata/1/pubpaa/04

7: /cgn2 6/ptodata/1/pubpaa/04

9: /cgn2 6/ptodata/1/pubpaa/04

10: /cgn2 6/ptodata/1/pubpaa/04

11: /cgn2 6/ptodata/1/pubpaa/04

12: /cgn2 6/ptodata/1/pubpaa/04

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17: /cgn2 6/ptodata/1/pubpaa/06

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20: /cgn2 6/ptodata/1/pubpa/06

20: /cgn2 6/ptodata
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(gn2 6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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(gn2 6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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US-09-954-571-3

US-09-954-571-4

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6 US-10-760-721-1

US-09-954-571-1

US-09-954-571-2

US-10-408-765A-478

6 US-10-705-791-1
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Sequence 1, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 14, Appl
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 478, App
Sequence 1, Appli
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-09-790-85	-10-495-148-4	0-495-148-	-10-282-122A-4	-10-104-047-355	-10-437-963-175	-10-723-860-38	9-769-736-	-10-282-122A-7	-10-767-701-	-10-760-72	-10-760-721-	-10-101-001-	-10-161-205-1	-09-491-614-	-09-259-658-1	-10-760-721-	-10-760-721-	0-760-721-	-10-873-594-2	-10-877-9	-10-815-514-2	-10-873-594-	-10-877-930-	0-815-514-	-10-724-532-2	-10-705-791-	-10-705-79	-10-705-791-	-10-705-791-1	-705-79	-10-705-791-	-10-705-791-	US-10-705-791-3
equence 7, App	nce 47, Ap	e 43,	ъф	equi	Sequence 175427,	Sequence 3853, Ap	Sequence 34, Appl	Sequence 73638, A	Sequence 42239, A	Sequence 5, Appli	Sequence 6, Appli	Sequence 17, Appl	Sequence 17, Appl	e 18, App	Sequence 19, Appl	e 3, Appl	2	e 4, Appl	25,	25,	25,	7, Appl	7,	7,	2, Appl	: 19, App	N	: 18, App	17, App	e 6, Appl	e 5, Appl	Sequence 4, Appli	e 3, Appl

ALIGNMENTS

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RESULT 2
US-09-954-571-3
; Sequence 3, Application US/09954571
; Publication No. US20020032167A1
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US-10-724-532-1
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                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARB: Patentin version 3.2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10724532
Publication No. US20040203027A1
GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
                                                                                                                                                                                               Query Match 100.0%; Score 150; DB 16; Best Local Similarity 100.0%; Pred. No. 2.2e-11; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: SR RPA
                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                             LENGTH: 30
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APPLICANT: Hoshijima, Masanıko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
APPLICANT: Ikeda, Yasuhiro
APPLICANT: Ikeda, Yasuhiro
CITILE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VETBION 3.2
SEQ ID NO 3
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TYPE: PRT
; ORGANISM: Canis familiaris
US-09-954-571-3
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                                                                                                                                                                                  Sequence 5, Application US/09954571 Publication No. US20020032167A1
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Best Local (
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Publication No. US20020032167A1
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Best Local Similarity
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APPLICANT: Ikeda, Yasuhiro
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
APPLICANT: ROSS, John
APPLICANT: IKedd, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
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APPLICANT: Hoshijima, Masahiko
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APPLICANT: Hoshijima, Masahiko
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APPLICANT: Hoshijima, Masahiko
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TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Pred. No. 3.7e-11;
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Pred. No. 3.7e-11;
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                                                                GENE TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 52;
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US-10-371-101-15
; Sequence 15, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
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APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590,7035.US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
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CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: GB 9912736.7
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SEQ ID NO 14
LENGTH: 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035.US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           1 QARQNLQNLFINFCLILICLLLICIIVMLL 30
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Pred. No. 3.7e-11;
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; PRIOR FILING DATE: 1999-06-01

; PRIOR APPLICATION NUMBER: 09/549,872

; PRIOR FILING DATE: 2000-04-14

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PATENTIN VEY: 2.0

SEQ ID NO 15

; ENGTH: 52

; TYPE: PRT
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US-09-954-571-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Slovic, Avram M.
APPLICANT: Summa, Christopher M.
APPLICANT: Summa, Christopher M.
APPLICANT: Saven, Jeffery G.
APPLICANT: DeGrado, William F.
APPLICANT: DeGrado, William F.
APPLICANT: Kono, Hidetoshi
TITLE OF INVENTION: Computational Design of a Water-Soluble Analog of a Protein, such
TITLE OF INVENTION: Se Phospholamban and Potassium Channel KCSA
FILE REFERENCE: 1694.0540001
CURRENT TPLILING DATE: 2004-01-23
RUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 53
TYPE: PRT
ORGANISM: Canine PLB
                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09954571 Publication No. US20020032167A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10760721 Publication No. US20040215400A1
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                     SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 52
TYPE: PRT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                  APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijam, Masahiko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
ORGANISM: Artificial
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Sequence 478, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:
APPLICANT: Fahy, Eoin D.
APPLICANT: Fahy, Eoin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glbenn, Bradford W.
APPLICANT: Glbenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Marnock, Dale B.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 478
LENGTH: 52
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; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-571-2
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; OTHER INFORMATION: Mutant form of humam protein sequence
US-09-954-571-1
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US-10-408-765A-478
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                                                                            ; ORGANISM: Homo sapiens 
US-10-408-765A-478
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Matches
Query Match
Best Local Similarity 96.7
Matches 29; Conservative
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Best Local Similarity 96.7%;
Matches 29; Conservative
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Publication No. US20020032167A1
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APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLS OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
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                                                                                                                 TYPE: PRT
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               96.0%;
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96.7%;
Score 144; DB 16;
Pred. No. 2e-10;
0; Mismatches 1;
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Pred No. 2e-10;
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Pred. No. 2e-10;
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US-10-705-791-3
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; ORGANISM: Homo sapiens
US-10-705-791-1
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                APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR APPLICAD DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
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Best Local Similarity
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
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SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR FAPPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
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PatentIn version 3.2
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Minamisawa, Susanne
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                                                                                                                                                                                                                                 Wang, Yibin
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96.7%;
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Pred. No. 2e-10;
0; Mismatches
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                                                                                                                                                                                                                                                                     RESULT 14
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-4
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US-10-705-791-4
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LENGTH: 52
TYPE: PRT
                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                               Sequence 5, Application US/10705791
Publication No. US20040121942A1
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
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TITLE OF INVENTION: METHOD FOR INHIBITION OF
TITLE OF INVENTION: OF CARDIAC DISEASE
                                                                                                                  APPLICANT:
 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                       1 QARQNLQNLFINFCLILICLLLICIIVMLL 30
I: Silverman, Gregg J.
INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
INVENTION: OF CARDIAC DISEASE
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                                                                             Hoshijima, Ma
Meyer, Markus
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Scott, Christopher
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Hoshijima, I
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                                                Scott, Chris
Wang, Yibin
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                                                                Christopher
                                                                                                Masahiko
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Pred. No. 2e-10;
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Pred. No. 2e-10;
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APPLICANT: Hoshijima, Masanıko
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CUURENT APPLICATION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: 60/106,718
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR PILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
SOFTWARE: SCO ID NOS: 19
SOFTWARE: SCO ID NOS: 19
SOFTWARE: SAtentin version 3.2
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens

OC 04. Scote 144; DB 16; Length 52;
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; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR PILING DATE: 1999-11-02
PRIOR PILING DATE: 1999-11-02
; PRIOR PILING DATE: 1999-13-02
; PRIOR PILING DATE: 1999-13-02
; PRIOR PILING DATE: 1999-13-02
; PRIOR FILING DATE: 1999-13-02
; PRIOR FILING DATE: 1999-13-02
; PRIOR SEQ ID NOS: 19
; SOFTWARE: PATENTIN VERSION 3.2
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PAT
; ORGANISM: Homo sapiens
US-10-705-791-5
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Search completed: July 7, 2005, 16:12:48 Job time: 386 secs
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Best Local Similarity
Matches 29; Conserv
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Publication No. US20040121942A1
GENERAL INFORMATION:
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APPLICANT:
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Hoshijima, Masahiko
Meyer, Markus
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Minamisawa, Susanne
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-QG-(gn2_1/USPTO_spool/US10724532/runat_07072005_100329_19987/app_query.fasta_1.199
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=blte -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10724532_@CGCN_1 1_4200_@runat_07072005_100329_19987 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEGUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Patent: JP 2002541859-A 9 10-DEC-2002;
DEVGEN NV
OS Sus sp. (pig)
PN JP 2002541859-A/9
PN JP 2002541859-A/9
PN 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PF 14-APR-1999 GB 9908670.4,15-APR-1999 US
O1-UN-1999 GB 9912736.7
PI RICHARD ZWAAL,JOSE GROENEN,THIERRY BOGAERT
PC C1201/42,C12N15/09,C12Q1/02,C12N15/00
CC Method for screening compounds
FH Key Location/Qualifiers
FT source 1.159
FT Source (pig)'.
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Sus sp.
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Zwaal,R., Groenen,J. and Bogaert,T.
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JP 2002541859-A/9.
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OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4,15-APR-1999 US
OI-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42,C12N15/09,C12Q1/02,C12N15/00
CC Description of Artificial Sequence:HUMANIZED
Key Location/Qualifiers
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FT Source 1.159
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1 (Dases 1 to 159)
Zwaal,R., Groenen,J. and Bogaert,T.
Method for screening compounds
Patent: JP 2002541859-A 13 10-DEC-2002;
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Zwaal,R., Groenen,J. and Bogaert,T.
Compound screening methods
Patent: US 6540996-A 13 01-APR-2003;
Location/Qualifiers
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Zwaal,R., Groenen,J. and Bogaert,T.
Compound screening methods
Patent: US 654096-A 9 01-APR-2003;
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Sequence 13 from Patent WO0063426
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                                                                                                  Zwaal, R., Groenen, J. and Bogaert, T. Compound screening methods Patent: WO 0063426-A 13 26-OCT-2000; Devgen NV (BE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sus sp."
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/mal_type="unassigned DNA"
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/db xrefe"texon:32630"
/noce="HUMANIZED PIG PLB cDNA"
                                                                                         ocation/Qualifiers
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Patent WO0063426.
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Rattus sp.
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
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phospholamban [rats, a
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                      156
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1 (bases 1 to 159)
Hwang, K.S. and Nadal-Ginard, B.
Cloning phospholamban cDNA from rat aortic smooth muscle
Adv. Exp. Med. Biol. 304, 387-395 (1991)
92206263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 95853] from the original journal article.
/codon_start=1
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/protein_id="AAB21903.1"
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ICIIVMLL"
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Housley,D.J.E., Ritzert,E. and Venta,P.J.
Comparative radiation hybrid map of canine
incorporating SNP and indel polymorphisms
Genomics 84 (2), 248-264 (2004)
2 (bases 1 to 314)
Housley,D.J.E., Ritzert,E. and Venta,P.J.
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AY514751
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Mammalia; I
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                                 TTGTTGATCTGCATCATTGTGATGCTTCTC
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199. .>314
/gene="PLN"
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                                                                                                                                                                                                                                                                                                                                                                              /gene="PLN"
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/protein_id="AAT44582.1"
/db_xref="GI:48476899"
/translation="MDKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL
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/number=2
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State University,
MI 48824-1314, USA
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RESULT 10
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Mammalia; E
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Rattus
S95849
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausmer, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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Location/Qualifiers
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Hwang, K.S. and Nadal-Ginard, B.

Cloning phospholamban cDNA from rat aortic
Adv. Exp. Med. Biol. 304, 387-395 (1991)
                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                         Mus musculus (house mouse)
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                                                  Mammalia; Eutheria;
1 (bases 1 to 648)
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                                                                                                                                                           IMAGE: 6772294),
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Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MEKVQYLTRSATRRASTIEMPQQARQNLQNLFINFCLILICLLL
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159. .317
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...386
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db_xref="taxon:10118"
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 53 Row: g Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12963502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94: Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (03-W2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Dr. Jonathan Kuo, NIMH cDNA Library Preparation: Michael Brownstein / Ted Usdin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
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Contact: MGC help desk
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                                                                                                                                                                         translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL"
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US-10-724-532-1 (1-30) x RNPHLAMB (1-701)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shanahan, C.M., Weissberg, P.L. and Metcalfe, J.C. Isolation of gene markers of differentiated and proliferating vascular smooth muscle cells Circ. Res. 73 (1), 193-204 (1993)
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X71068.1 GI:313809
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Dept of Biochemistry, Tennis
Location/Qualifiers
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.norvegicus mRNA for phospholamban.
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                                                                                                                                                                                                                                                                                                                                                                                       organism="Rattus"
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                                                                                                                                                                                                                                                                                    /dev_stage="adult"
|74._.332
                                                                                                                                                                                                                                                                                                                tissue type="aorta smooth muscle"/clone_Tib="lambda-Zap"
                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                             clone="2RB7"
                                                                                                                                                                                                                                                                                                                                                                           strain="Wistar"
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Submitted (13-APR-1989) Eggermont J.A., Laboratorium Voor
Fysiologie K.U. Leuven, Campus Gasthuisberg O/N, Herestraat 49,
B-3000 Leuven, Belgium
See < 100399> for canine phospholamban and < 100761> for rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Verboomen,H., Wuytack,F., Eggermont,J.A., De Jaegere,S.,
Missiaen,L., Raeymaekers,L. and Casteels,R.
cDNA cloning and sequencing of phospholamban from pig stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (pig)
Sus scrofa
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Pig mRNA for phospholamban.
X15075
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Eggermont, J.A.
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   LeuLeuIleCysIleIleValMetLeuLeu
                                               GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu
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                                                                                                                                                                                                                                                      note="polyA site"
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Cetartiodactyla; Suina; Suidae;
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Sus.
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Canis sp.
Canis sp.
                                                                                                                                                                                                                                                                                                                              21
                                                                Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleoscon Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 832)

Uyeda,A., Kitano,K., Fujii,J., Kadoma,M., Tada,M. and Tanaka,S. Characterization of recombinant cDNA clones for canine cardiac
                                                                                                                                                                                                        Dog cardiac phospholamban mRNA, M35393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (Dases 1 to 832)

Fujii,J., Ueno,A., Kitano,K., Tanaka,S., Kadoma,M. and Tada,M. Complete complementary DNA-derived amino acid sequence of canine cardiae phospholamban

cardiae phospholamban

J. Clin. Invest. 79 (1), 301-304 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phospholamban.
Canis lupus (gray wolf)
Canis lupus
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Canine cardiac
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Location/Qualifiers
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                                                          phospholamban
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ICIIVMLL"
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l81. .339
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Dog heart,
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Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 858)
Fujii,J., Zarain-Herzberg,A., Willard,H.F., Tada,M. and
MacLennan,D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rabbit phospholamban gene, partial exon M63601 GI:165636 phospholamban gene, partial exon M63601.1 GI:165636
                                                                                                                                                                                                                                                                                                                                           Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6 J. Biol. Chem. 266 (18), 11669-11675 (1991) 91268032
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Location/Qualifiers
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2 of 3
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181. .339
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428. .858
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                                          590
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             LeuLeuIleCysIleIleValMetLeuLeu 30
                                         CAAGCACGTCAAAACCTCCAGAACCTATTTATCAATTTCTGTCTCATCTTGATATATGTCTC 649
                                                      GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu
CTGCTGATCTGCATCATCGTCATGCTTCTC 679
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-Q-/cgn2 1/USPTO_spool/US10724532/runat_07072005_100329_19999/app_query.fasta_1.199
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX:100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10724532 @CGN 1 1 4352 @runat 07072005 100329 19999 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AAB39963 VW66E09.r

AA655419 VV14D04.r

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AA439318 Vf42E04.r

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ALIGNMENTS

	PUBMED COMMENT	JOURNAL MEDLINE	AUTHORS TITLE	e de	KEYWORDS SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 BE113353/c LOCUS DEFINITION
Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA 7el: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) Seq primer: M13 Forward POLYA=No.	8889548 Contact: Soares, MB	discovery Genome Res. 6 (9), 791-806 (1996) 97044477	Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	EST. Rattus norvegicus (Norway rat) Rattus norvegicus	UI-R-BJI-awe-d-04-0-UI 3', mKNA sequence. BE113353 BE113353.1 GI:8505458	BE113353 179 bp mRNA linear EST 13-JUN-2000 UI-R-BJ1-awe-d-04-0-UI.81 UI-R-BJ1 Rattus norvegicus cDNA clone

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VERSION
KEYWORDS
SOURCE
ORGANISM
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AA462116
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JOURNAL
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                                                                                                    Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston,R.
The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                      Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dul
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EST.
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5' similar to
Trace considered overall poor quality
                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                      Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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/lab host="PH10B (Life Technologies)"
/clone lib="UI-R-BJI"
/clone lib="UI-R-BJI"
/clone lib="UI-R-BJI"
/clone lib="UI-R-BJI"
/clone lib="UI-R-BJI"
/clone lib="UI-R-BJI"
/clone lib="Vector: pT73D3-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJI library is a subtracted library derived from the following tissues: atrium at 16.5 dpc, ventricle at 16 5 dpc, AV canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, available to 15 dpc, available to 15 dpc, available to 15 dpc, and adult heart. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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to gb:M63603
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NbMH Mus musculus cDNA clone IMAGE:871527
CARDIAC PHOSPHOLAMBAN (HUMAN);, mRNA
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Query Match:
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                                                                                                                                                                                          1 (bases 1 to 328)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubus,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                          AA839963

vw66f09.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
IMAGE:1259945 5' similar to gb:M63603 CARDIAC PHOSPHOLAMBAN
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further;
                                                                              WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                               Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                          AA839963.1 GI:2916557
                                                                                                                                Contact: Marra M/Mouse EST Project
                                                                                                                                             Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                        (HUMAN);,
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Location/Qualifiers
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/lab_host="DH108"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:871527"
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Matches:
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    μ
                                                                                 Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
                                                                                                                                                                                                                      1 (bases 1 to 331)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuc, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA655419 331 bp mRNA linear EST 04-NOV-1997 vv14b04.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE: 1211599 5' similar to gb:M63603 CARDIAC PHOSPHOLAMBAN
                           Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                    AA655419
AA655419.1 GI:2591573
EST.
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Location/Qualifiers
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Seq primer:
MGI:647943
Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMAN);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="NIH Swiss"
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'mol type="mpwa"
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Nikasido, I., Osato, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikasido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Della, E., Dragani, T.A., Chothia, C., Corbani, L.B., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Varang, L., Walning, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yan
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BY149365 RIKEN full-length enriched, 17.5 days embryo whole body
Mus musculus cDNA clone L930261L14 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
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/note="Organ: heart, Vector: pBluescript SK; Site 1:
EcoRI, Site 2: XhOI; Cloned unidirectionally. Primer:
Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZhP XR Vector; ~5'
adaptor sequence: 5' GANTTTTTTTTTTTTTTTT 3'"
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
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/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
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/gtrain="NIH Swigg"
/db_xref="taxon:10090"
/clone="IMAGE:1211599"
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Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1777-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome
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                              LeuLeuIleCysIleIleValMetLeuLeu 30
                                                                                                                                                GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="L930261L14"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
whole body"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                      209
μ
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Porest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuc
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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5′ similar
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1 (bases 1 to 347)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Location/Qualifiers
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
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                                                                            GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                        provided by
                                                                                                                                                                                                                                                                                                                                    constructed
                                                                                                                                                                                                                                                                                                                                                      3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE:846463"
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NbMH Mus musculus cDNA clone IMAGE:846463
CARDIAC PHOSPHOLAMBAN (HUMAN);, mRNA
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                                                                                                                                                                Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Fax: 81-45-503-9216
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                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 362)

Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M.,
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                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome
                                                                    Tel: 81-45-503-9222
                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
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Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                 Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 366)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)
                                                                                                                                      FMax: J14 200 10.20 Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                      Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIS97561 366 bp mRNA linear EST 21-APR-19 vd80e10.y1 Soares mouse NbMH Mus musculus cDNA clone IMAGE:806922 5' similar to gb:M63603 CARDIAC PHOSPHOLAMBAN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                 MGI:483266
This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuLeuIleCysIleIleValMetLeuLeu 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTGATCTGCATCATTGTGATGCTTCTG
                                        primer: -40RP from Gibco.
                                                                                                                                                                                                                   314 286 1800
314 286 1810
                                                             orientation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref="taxon:10090"
'clone="L930045G09"
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ACCESSION
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KEYWORDS
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AA499852
LOCUS
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 CAAGCACGTCAGAATCTCCAGAACCTATTTATCAATTTCTGCCTCATCTTGATATGTCTG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 CTGCTGATCTGCATCATTGTGATGCTTCTG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free tl
IMAGE Consortium (info@image.llnl.gov)
                                                                                             Unpublished (1996)
Contact: Marra M/Mouse EST Project
Contact: Marra M/Mouse EST Project
Washbu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                            1 (bases 1 to 369)
Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubigeisel, S., Kuchba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                             Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA499852.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               vg05g01.rl
5' similar
High quality sequence stop: 320
Location/Qualifiers
                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA499852
                                  MGI:504584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dev_stage="4 weeks"
/lab_host="DH10B"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soares mouse
to gb:M63603
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100.00%
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 bp mRNA linear EST 01-J
NbMH Mus musculus cDNA clone IMAGE:8
CARDIAC PHOSPHOLAMBAN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus"
                                                   royalty-free through LLNL ; contact the image.llnl.gov) for further information.
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Matches:
Conservative:
Mismatches:
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ACCESSION
VERSION
KEYWORDS
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CB041339
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Best Local Similarity:
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DEFINITION
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                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 373)
dd Mota,A.F., Sonstegard,T.S., Van Tassell,C.P., Matukumalli,L.K.,
Wood,D.L., Capuco,A.V., Brito,M.A.P., Martinez,M.L., Connor,E.E.,
Machado,M.A. and Coutinho,L.L.
Construction and Characterization of cDNA Libraries Generated from
Mammary Gland Tissues of Holstein (Bos taurus) and Gir (Bos
                                                                                                                                                                                                                                                                                                        Bos indicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                 Unpublished (2002)
Contact: Adilson F. da Mota
Contact: Adilson F. da Mota
Gene Evaluation and Mapping Laboratory
USDA, ARS, Animal and Natural Resources
Bldg. 200 Rm3 BARC-East, Beltsville, MD
Tel: 3015048456
Fax: 3015048414
                                                                                                                                                                                                                                                                                                                                                                                   Unknown, mRNA sequence.
CB041339
CB041339.1 GI:27760584
EST.
Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt '' -trim_fasta. Vector identified by cross_match using options -minmatch 12 -minscore 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                      4003081 BARC-EMBRAPA 312BOV
                                                                                                                                                                                                                                                                                                     Bovinae; Bos.
                                                  Email: amota@cnpgl.embrapa.br
                                                                                                                                                                                 indicus) Cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu
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                                                                                                                                                                                                                                                                                                                                                                   indicus (zebu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:860496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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150.00
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Matches:
Conservative:
Mismatches:
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Gaps:
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Bos indicus cDNA clone 312BOV_1A09
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                                                                                                    Institute
20705, USA
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SOURCE
ORGANISM
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KEYWORDS
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BY092385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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CE 1 (bases 1 to 375)

RS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schombach, Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Hane, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gassterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 CAAGCACGTCAAAATCTCCAGAACCTATTTATCAATTTCTGTCTCATCTTAATATGTCTC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 bp mRNA linear EST 07-
BY092385 RIKEN full-length enriched, 10 days meonate heart
musculus cDNA clone K630091G17 5', mRNA sequence.
BY092385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: 1 row: A column: 09
Seq primer: GTTTTCCCAGTCACGATG
High quality sequence stop: 373.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: GTTTTCCCAGTCACGACGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuLeuIleCysIleIleValMetLeuLeu 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="BARC-EMBRAPA 312BOV"
/note="Organ: mammary; Vector: pUC19; Site 1: SmaI;
Site 2: SmaI; This mammary-derived cDNA library was
created as part of a collaborative project between the AR
Gene Evaluation and Mapping Laboratory and the EMBRAPA
Dairy Cattle Research Center under the sponsorship of
USDA, ARS/EMBRAPA-LABEX program in animal genomics RNA
extracted on 6/8/02 with Invitrogen Superscript II at 37
deg C annealing temperature."
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/mol_type="mRNA"
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/cell_type="multiple"
/dev_stage="involuted"
/lab_host="K-12"
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/strain="Brazilian Dairy
/strain="Brazilian Dairy
/db xref="taxon:9915"
/clone="31280V 1A09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                  /tissue_type="heart"
/dev stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LINL (info@image.llnl.gov). IMAGE ID= 1789595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 5224
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UI-R-C2p-rc-e-01-0-UI.rl UI-R-C2p Rattus norvegicus cDNA clone
UI-R-C2p-rc-e-01-0-UI 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/clone lib="UI-R-C2p"

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'lab_host="DH10B (Life Technologies)"
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CONTACT: Lewin, H. A.
CONTACT: Lewin, H. A.
M. Mckck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutaleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                     Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g:
Cross match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF044741 378 bp mRNA linear BP250001B10F7 Soares normalized bovine placenta Bos clone BP250001B10F7 5', mRNA sequence.
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                                                                                                                                                                                                                                                                  quality sequence stop: 378.
Location/Qualifiers
/clone lib="Soares normalized bovine placenta"
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Site_2: Not1; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "
                                                                                                                                                           /mol_type="mRNA"
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                                                                                                                     'lab_host="DH10B"
                                                                                                                                                                                                                         organism="Bos taurus"
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Elkaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
RE 1 (bases 1 to 378)

RS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yemanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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Hume, D. A., Oquackenbush, J., Schriml, L.M., Kanapin, A.,
Hatsuda, H., Baldar, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaastearland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Bradt, D., Brusic, V.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Pettovsky, N., Pillai, R., Pontius, J. U., Ql, D., Ramachandran, S.,
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Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Watlana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Watshawa, T., Konno, H., Nakamura, M.,
Yang, I., Yun, J., Sato, K., Sahi, Y., Sahara, M., Yang, I.,
Nakamara, J., Khida, S., Hara, A., Hashizume, W., Inotani, K., Ishii, Y.,
Ishii, Y.,
Shibata, Y.,
Shiba
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                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
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genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
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Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
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Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
                                                                                                                296
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                                                                                                                                            21 LeuLeuIleCysIleIleValMetLeuLeu 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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heart"
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-MODEL-frame+ p2n.model -DEV-xlh
-Q-/cgn2 1/USPTO_spool/US10724532/runat_07072005_100330_20013/app_query.fasta_1.199
-Q-/cgn2 1/USPTO_spool/US10724532/runat_07072005_100330_20013/app_query.fasta_1.199
-DB=Issued_Patents NA -QFMT-£astap -SUFFIX=p2n.rni -MINMAYCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST-45 -DOCALIGN=200 -THR SCORE-pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-sext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10724532 @CGN 1 1 177 @runat 07072005 100330 20013 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                Score
        1444
130
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68
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66
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seq length: 2000000000
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , I
      100.0
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2 6/ptcdata/1/ina/5A_COMB.seq:*
/cgn2 6/ptcdata/1/ina/5B_COMB.seq:*
/cgn2 6/ptcdata/1/ina/6A_COMB.seq:*
/cgn2 6/ptcdata/1/ina/6B_COMB.seq:*
/cgn2 6/ptcdata/1/ina/6B_COMB.seq:*
/cgn2 6/ptcdata/1/ina/backfles1.seq:*
                                                                                                                                                                                                                                                            Length
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Ygapext
Fgapext
Delext
US-09-549-872B-9

US-09-549-872B-13

US-09-513-999C-10799

US-09-949-016-13381

US-09-949-016-13181

US-09-124-671-26

US-09-124-671-15638

US-09-270-767-10524

US-09-270-767-11139

US-09-270-767-14139

US-09-949-016-12461

US-09-949-016-12461
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  Sequence 9, Appli
Sequence 13, Appl
Sequence 10799, Ap
Sequence 1439, Ap
Sequence 25, Appl
Sequence 15638, A
Sequence 10524, A
Sequence 11139, A
Sequence 14599, A
Sequence 12461, A
Sequence 12461, A
Sequence 16853, A
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10 10 10 10 10 10 10			
844448 8444	200644, 200790, 16237, A 13345, A 12219, A 15242, A 12086, A	2777 3753 7163 7163 7266 6078 6078	

ALIGNMENTS

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APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogeart, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
                                        Percent Similarity:
Best Local Similarity:
                                                                                                     Pred. No.:
                     Query Match:
                                                                                   Score:
                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                SOFTWARE: PatentIn SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09549872B Patent No. 6540996 GENERAL INFORMATION:
                                                                                                                                                                                TYPE: DNA
ORGANISM: Sus sp.
                                                                                                                                                                                                                             LENGTH: 159
                 4.89e-12
150.00
100.00%
100.00%
                   Conservative: Mismatches: Indels:
Gaps:
0 30 0
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US-10-724-532-1 (1-30)

x US-09-549-872B-9 (1-159)

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APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
APPLICANTION IExpressed Sequence Tags and
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION UMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: DO0590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR PILING DATE: 1999-66-01
NUMBER OF SEQ ID NOS: 39
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 13
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                Sequence 10799, Application US/09513999C Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
  SEQ ID NO 10799
                                                                                                                                                                                                 APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 159
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PRILING DATE: 2000-10-20
PRIOR PRILING DATE: 2000-10-3
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1439
US-09-949-016-13181
; Sequence 13181, Applic
; Patent NO. 6812339
; PATENTAL INFORMATION:
; APPLICANT: VENTER, J.
; TITLE OF INVENTION: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-10799
                                                                                                                       RESULT 5
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Best Local Similarity:
Query Match:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1635
TYPE: DNA
ORGANISM: Human
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                                                                                                                                                              308 TIGCIGATOTGTATCATOGTGATGCTTCTC
                                                                                                                                                                                                                                             248 CAAGCACGTCAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCATCTTAATATGTCTC
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                                                                                                                                                                                                                                                                 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
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                                                                                Application US/09949016
                        <u>.</u>
    J. Craig et al.
POLYMORPHISMS
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      IN KNOWN GENES
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Matches:
Conservative:
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Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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OF DETECTION AND
          ASSOCIATED
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24 CysileIleValMetLeuLeu 30
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Sequence 26, Application US/09124671A
Patent No. 616008
GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-09-08
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; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10524
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEG ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10524
LENGTH: 490
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SEQ ID NO 15638
LENGTH: 69764
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(69764)
OTHER INFORMATION: n = A,T,C
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; SEQ ID NO 14599
; LENGTH: 992
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14599
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GENERAL INFORMATION:
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                                                                                                                                                             APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILLNG DATE: 199-03-17
NUMBER OF SEQ ID NOS: 62517
SOPTWARE: Patentin Ver. 2.0
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TYPE: DNA
ORGANISM: Drosophila melanogaster
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US-09-949-016-12461
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SOFTWARE: FastSEQ for
SEQ ID NO 12461
                                                                                                                                                                                                                                                          Sequence 16853, Applica
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J.
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GENERAL INFORMATION:
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CURRENT ADDITION:
                                                          CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012
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RESULT 14
US-09-949-016-15563
; Sequence 15563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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DB:
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
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US-09-949-016-136216/c
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Best Local Similarity:
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SEQ ID NO 16853
LENGTH: 93920
TYPE: DNA
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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TYPE: DNA
ORGANISM: Human
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; NAME/KEY: misc feature

; LOCATION: (1)...(202001)

; OTHER INFORMATION: n = A,T,C

US-09-734-674-3
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US-10-724-532-1 (1-30) x US-09-734-674-3 (1-202001)
                                                                                                                                        Pred. No.:
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US-09-734-674-3/c
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SEQ ID NO 3
FORGTH: 202001
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PELICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09734674
Patent No. 6498022
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WEI, Ming-Hui et all TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: UCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: CLOOIO18
FILE REFERENCE: CLOOIO18
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                            LENGTH: 202001
TYPE: DNA
ORGANISM: Human
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SOFTWARE: FastSEQ for
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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ORGANISM: Human
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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-Q-(gn2 1)USFTO spool/US10724532/runat 07072005 100331_20083/app_query.fasta_1.199
-Q-(gn2 1)USFTO spool/US10724532/runat 07072005 100331_20083/app_query.fasta_1.199
-DBs-Published_Applications_NA _OFMT=fastap_SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANUS=hunan40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10724532 @CGN 1 741 @runat 07072005 100331 20083
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NGE_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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           July 7, 2005, 18:51:35; Search time 415 Seconds (without alignments)
453.854 Million cell updates/sec
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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/ Cgn2_6/ptodata/1/pubpna/US09E PUBCOMB.seq: *
/ Cgn2_6/ptodata/1/pubpna/US09E PUBCOMB.seq: *
/ Cgn2_6/ptodata/1/pubpna/US09E PUBCOMB.seq: *
/ Cgn2_6/ptodata/1/pubpna/US09C PUBCOMB.seq: *
/ Cgn2_6/ptodata/1/pubpna/US09C PUBCOMB.seq: *
/ Cgn2_6/ptodata/1/pubpna/US10E PUBCOMB.seq: *
/ Cgn2_6/ptodata/1/pubpna/US10I PUBCOMB.seq: *
/ Cgn2_6/ptodata/1/pubpna/US10I NEW PUB.seq: *
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/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
-6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	Match	Length	BB	ID	jģt
_	150	8			S-10-371-101-9	е і
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ი (144		1635	21	0-843-641A-1	equenc
7		Ü,	9		-09-918-995-4	quenc
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	137	Ë	w		-10-724-532-6	equenc
_	130	6	\vdash		-10-815-514-2	Sequence
16	130	9	\vdash	20	-10-877-930-2	equenc
		6	315	21	10-873-594-26	Sequence
	117	8	9	10	-09-918-995-173	equenc
		٠.٠	40	10	-09-918-995-	equenc
	68	٠	N	13	-10-087-192-451	equenc
	5 5	u.	ຸ່ດ	20	-10-357-930-53	equenc
אנ	n 01	בי גול גול בי	4322	; ;	-10-087-192-51	equenc
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			7	16	US-10-312-841-1	Sequence
	σ,	N	1368	8	US-10-424-599-5	Sequence
N		42.0	89	20	-10-739-930-303	Sequence
N		'n	0200		9-734-674-3	quence
	2 6	42.0	100202	24	US-10-2/4-990-3	Sequence
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	Ν,	۲	9765		9-813-320-3	Sequence 3
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, ω , 4	5 62	41.3	409	19	-10-674-124A-	quenc
		٠.	4.6	19	-10-674-124A-564 -10-331-714A-501	Sequence
		41.3	34769	18	-10-221-714A-50 -10-333-696-157	equenc
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		٠:	7000	3 5	-10-067-192-99	Anerro
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٠.	61	0 9	605	1	10-027-632-6326	Sequence
43		40.7	0		-10-027-632-632	Sequence
44	61	40.7	N	13	-10-027-632-28030	Sequence
45	61	40.7	623	17	10-027-632-280	Sequence
					ALIGNMENTS	
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RESULT 1	1 71-101-9					
		Applicat No. US20	ion US 030149	/1037 995A1	71101	
, APPLICA	Į.					
APPLI	LICANT	Groenen	10086	į		
; TITLE	윾	INVENTION:	COMPOU	S S	CREENING METHODS	
; FILE	Ę	CE: D005	1590.70035		S	
CURRENT	g g	PLICATION DATE:	Z	-02-	3/10/371,101	
, PRIOF	Ĕ,	ğ	NUMBER:	۳;		
PRIOR	RFILING		. 5	ທ	0/100 50	
; PRIOR ; PRIOR	R APPLICATION R FILING DATE:		NUMBER: 1999-04	-15 US 6	0/129,596	

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Sequence 13, Application US/10371101

Publication No. US20030149995A1

GENERAL INFORMATION:

APPLICANT: Zwaal, Richard

APPLICANT: Groenen, Jose

APPLICANT: Bogaert, Thierry

TITLE OF INVENTION: COMPOUND SCREENING METHODS

FILE REFERENCE: D00590.70035.US

CURRENT APPLICATION NUMBER: US/10/371,101

CURRENT FILING DATE: 2003-02-21

PRIOR APPLICATION NUMBER: US 60/129,596

PRIOR APPLICATION NUMBER: US 60/129,596

PRIOR APPLICATION NUMBER: US 60/129,596

PRIOR APPLICATION NUMBER: GB 9912736.7

PRIOR FILING DATE: 1099-06-01

PRIOR FILING DATE: 1099-04-14

NUMBER OF SEQ ID NOS: 39
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; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9
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                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-371-101-13
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                                                           US-10-724-532-1 (1-30) x US-10-371-101-13 (1-159)
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 13
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PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 159
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity:
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1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu
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Indels:
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2041-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 4045
LENGTH: 525
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; LENGTH: 159
; TYPE: DNA
; ORGANISM: Human
US-10-691-412-1
                                                                                                       ; FEATURE:
, NAME/KEY: misc feature
, LOCATION: (1)...(525)
, OTHER INFORMATION: n =
US-09-918-995-4045
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                Percent Similarity:
                                                                     Alignment Scores:
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US-09-918-995-4045
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Query Match:
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Best Local Similarity:
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APPLICANT: Kranias, Evangelia G.
APPLICANT: Kobra, Haghighi
APPLICANT: Kobra, Haghighi
TITLE OF INVENTION: Phospholamban Polymorphisms and Methods of Assessment
FILE REFERENCE: 10738-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4045, Application US/09918995
Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10691412
Publication No. US20040191802A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/691,412
CURRENT FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                 ORGANISM: Homo sapiens
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APPLICANT: EBner, Reinhard
APPLICANT: Carter, Kenneth
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT PILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR APPLICATION NUMBER: U.S. 60/245,084
PRIOR APPLICATION NUMBER: U.S. 60/245,084
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Best Local Similarity:
Query Match:
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US-10-843-641A-162
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-162
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US-09-873-367C-162
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Sequence 162, Application US/10843641A
Publication No. US20050064454A1
GENERAL INFORMATION:
APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 699290-189
CURRENT APPLICATION NUMBER: US/10/843,641A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 162, A Publication No.
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No.:
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Augustus, Meena
Ebner, Reinhard
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o. US20030165839A1
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GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4217

LENGTH: 394
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Best Local Similarity:
Query Match:
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US-09-918-995-4217
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; ORGANISM: Homo
US-10-843-641A-162
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PRIOR FILLING DATE: 2001-09-25
PRIOR PELLORITION NUMBER: US/09/962,832
PRIOR PELLORITION NUMBER: US/09/964,832
PRIOR PELLORITION NUMBER: US/09/964,824
PRIOR PELLORITION NUMBER: US/09/964,824
PRIOR PELLORITION NUMBER: US/09/967,768
PRIOR APPLICATION NUMBER: US/09/968,007
PRIOR APPLICATION NUMBER: US/09/968,007
PRIOR APPLICATION NUMBER: US/09/969,347
PRIOR PILLING DATE: 2001-10-02
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SEQ ID NO 162
LENGTH: 1635
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Publication No. US20030073623A1
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(394)
OTHER INFORMATION: n = A,T,C
-09-918-995-4217
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PRIOR APPLICATION NUMBER: US/09/873,367
PRIOR FILING, DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US/09/954,531
PRIOR APPLICATION NUMBER: US/09/954,456
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/09/954,456
PRIOR FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 8447
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                                                                                                                                           TYPE: DNA
                                                                                                                ORGANISM: Homo sapiens
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APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 2041-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTMARE: FastSEQ for Windows Version 3.0

SEQ ID NO 5377
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Best Local Similarity:
Query Match:
DB:
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US-09-918-995-3950
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, NAME/KEY: misc feature
; LOCATION: (1) ... (487)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-5377
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US-09-918-995-5377
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
                                                                                                                            Sequence 3950, Application US/09918995 Publication No. US20030073623A1
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TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5235
LENGTH: 418
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                     US-10-724-532-1 (1-30) x US-09-918-995-5235 (1-418)
                                                                                                                                                        Query Match:
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Best Local Similarity:
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US-09-918-995-5235
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Best Local Similarity:
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NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FREUSEQ for Windows Version 3.0
SEQ ID NO 3950
LENGTH: 380
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5235, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(418)
OTHER INFORMATION: n = A,T,C
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LOCATION: (1)...(380)
OTHER INFORMATION: n = A,T,C or G
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21 LeuLeuIleCysIleIleValMetLeuLeu 30
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US-10-724-532-4/c
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; ORGANISM: mus musculus
US-10-724-532-3
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US-10-724-532-3
                                               US-10-724-532-1 (1-30) x US-10-724-532-4 (1-108)
                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10724532
Publication No. US20040203027A1
GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic TITLE REFERENCE: SR RPA CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT PILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US/60/430322
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 108
TYPE: DNA
ORGANISM: mus musculus
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                                                                                                                                                        No . .
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1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu
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Percent Similarity:
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Query Match:
DB:
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US-10-724-532-6/c
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US-10-724-532-5
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                                                                                                                                                                                                                                                    Sequence 6, Application US/10724532
Publication No. US20040203027A1
GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-02
PRIOR FILING DATE: 2003-12-02
PRIOR FILING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 135
TYPE: DNA
ORGANISM: mus musculus
                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10724532 Publication No. US20040203027A1
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TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo) plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT APPLICATION NUMBER: US 60/430322
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
PRIOR FILING DATE: 2002-12-02
PRIOR PILING DATE: 2002-12-02
PRIOR PILING DATE: 2002-12-02
                                                                                                                                                   TYPE: DNA
ORGANISM: mus musculus
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93.33%
91.33%
3.49e-09
137.00
93.33%
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Conservative:
Mismatches:
Indels:
                   Conservative: Mismatches: Indels:
Gaps:
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Matches:
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RESULT 15

US-10-815-514-26

Sequence 26, Application US/10815514

Publication No. US20040204361A1

GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Hoe, Mee

TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT FILING DATE: 2004-03-31
PRIOR APPLICATION NUMBER: US/10/815,514
CURRENT FILING DATE: 2000-10-26

NUMBER OF SEQ ID NOS: 42
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 315
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chimeric human PLB-KDEL
US-10-815-514-26
                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
Search completed: July 7, 2005, 20:34:06
Job time : 424 secs
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                                                                            24 CysIleIleValMetLeuLeu 30
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                                                           TGTATCATCGTGATGCTTCTC 180
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: 9b ba:*
2: 9b ht9
3: 9b in
4: 9b or
5: 9b c
6: 9b c
7: 9b 7
9: 9
 seq length: 0 seq length: 2000000000
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1 atgcatgagagaaggcctca.....gcattatcgtcatgctcctg
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1786
223728
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2841
159
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 2110
       RABPHLAM2
OCPHLAM
BD247907
BD247911
AR302007
AX040487
AX040487
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RNPHLAMB
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AC097906
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                       M63601 Rabbit phos
700761 O.cuniculus
BD247901 Method fo
AB247911 Method fo
AR302003 Sequence
AR302003 Sequence
AX040491 Sequence
AX040491 Sequence
AX040491 Sequence
X15075 pig mRNA fo
S95853 phospholamb
S95849 Rattus sp.
X71068 R. norvegicu
L03382 Rat phospho
AC023956 Rattus no
AC128365 Rattus no
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BC061097 Mus muscu
S46792 phospholamb
AC100317 Mus muscu
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ï	46.8	43.3		ഗ	BX537355	BX537355 Zebrafish
Ñ	46.4	43.0		v	CHKPLB	M59039 Chicken car
ü	46.4	43.0	3423	v	CHKPLB2	
4.	46	42.6	306	σ	CQ447405	CQ447405 Sequence
ű	46	42.6	323	9	HUMPLAM	M60411 Human phosp
õ	46	42.6	480	δ	AX894936	AX894936 Sequence
7	46	42.6	480	0	BD030469	BD030469 Sequence
œ	46	42.6	980	9	HSPLBG2	
ö	46	42.6	1635	σ	CQ718671	CQ718671 Sequence
ō	46	42.6	1635	o	AX329653	AX329653 Sequence
ü	46	42.6	1635	9	нименцам	M63603 Human phosp
Ñ	46	42.6	1691	9	BC005269	Homo
ũ	46	42.6	60797	N	AL355356	AL355356 Homo sapi
4	46	42.6	66092	N	AL136974	АL136974 Ното варі
ű	46	42.6	150290	9	HS509L4	Z99496 Human DNA 8
ð	44.4	41.1	314	4.	AY514751	AY514751 Canis fam
J	44.4	41.1	832	4	DOGPHL	
œ	44.4	41.1	832	4	DOGPLBA	M35393 Dog cardiac
Ö	44.4	41.1	2614	4	CFPHLX	Y00399 Dog phospho
Ö	43.6	40.4	315	o	AR121629	
μ	36	33.3	147419	ø	HS738P11	AL031736 Human DNA
N	Ü	30.7	204114	N	AC108810	AC108810 Mus muscu
ũ	KA.	30.4	1593	9	AK098521	AK098521 Homo sapi
4	•	30.4	1893	9	HSHR21SPA	X98294 Homo sapien
Ğ	J				DK105600	AK125620 Homo sapi

ALIGNMENTS

ORIGIN	CDS	exon	mRNA	source	FEATURES	COMMENT	JOURNAL	TITLE	REFERENCE AUTHORS		SOURCE ORGANISM	KEYWORDS SEGMENT	ACCESSION VERSION	DEFINITION	RABPHLAM2
Ca-ATPase" /cadon_start= /codon_start= /codon_start= /codon_start= /codon_start= /product="phospholamban" /protein_id="AAA31445.1" /protein_id="AAA31445.1" /bb_xref="GI:165639" /translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL ICIIVMLL"	<pre>/product="phospholamban" /number=2 524682 /function="regulatory protein of sarcoplasmic reticulum</pre>	/product="phospholamban" 428858	/organism="oryclolagus cunicules" /mol_type="genomic DNA" /db xref="taxon:9986" /tiBaue_lib="rabbit genomic" join(M63600.1:855943,428858)		Location/Qualifiers	1828805 Original source text: Rabbit DNA.	CDMA, and assignment of the gene to indust curcinosome of J. Biol. Chem. 266 (18), 11669-11675 (1991) 91268032	MacLennan, U.H. Structure of the rabbit phospholamban gene, cloning of the human	1 (bases 1 to 858) Fujii, J., Zarain-Herzberg, A., Willard, H.F., Tada, M. and	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	Oryctolagus cuniculus (rabbit) Oryctolagus cuniculus	#	M63601.1 GI:165636	phospholamban gene, partial exon 2.	מת

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KEYWORDS
SOURCE
ORGANISM
                                                          KEYWORDS
SOURCE
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BD247907
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AUTHORS
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Matches 71
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Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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l Similarity 69.6%;
71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCPHLAM
O.cuniculus mRNA for phospholamban.
Y00761
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 159)
                                                                                               BD247907 159 bp Method for screening compounds.
BD247907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 2841)
Fujii, J., Lytton, J., Tada, M. and MacLennan, D.H.
Rabbit cardiac and slow-twitch muscle express t
                                            de ap.
                                                                      BD247907.1 GI:33057677 JP 2002541859-A/9.
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FEBS Lett. 227 (1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y00761.1 GI:1661
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/product="phospholamban"
/protein_id="CAA68730.1"
/db_xref="GI:1662"
/db_xref="GOA:P20006"
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/db_xref="UniProt/Swiss-Prot:P20006"
/translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Oryctolagus"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                             48.5%;
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Pred. No. 2.2e-06;
0; Mismatches 31;
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Pred. No. 2.5e-06;
0; Mismatches 31;
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    Matches
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REFERENCE
AUTHORS
TITLE
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ACCESSION
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KEYWORDS
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BD247911
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Method for screening compounds

Patent: JP 2002541859-A 9 10-DEC-2002;

DEVCEN NV

OS Sus sp. (pig)
PN JP 2002541859-A/9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PF 14-APR-1999 GB 9908670.4,15-APR-1999 US
01-UN-1999 GB 9912736.7
PI RICHARD ZWAAL,JOSE GROENEN,THIERRY BOGAERT
PC C1201/42,C12N15/09,C1201/02,C12N15/00
CC Method for screening compounds
FH Key
FT source 1.159
FT source 1.159
FT source 1.159
                                                                                      DEVGEN NV
OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PF 14-APR-1999 GB 9908670.4,15-APR-1999 US 60
PR 15-APR-1999 GB 9912736.7
PI RICHARD ZWAAL,JOSE GROENEN,THIERRY BOGAERT
PC C1201/42,C12N15/09,C1201/02,C12N15/00
CC Description of Artificial Sequence:HUMANIZED PIC
Key Location/Qualifiers
FT source 1. 159
FT source 1. 159
FT source 1. 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 CTTAATATGCCTCTTGCTGATTTGCATCATCGTGATGCTTCT
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Zwaal, R., Groenen, J. and Bogaert, T.
Method for screening compounds
Patent: JP 2002541859-A 13 10-DEC-2
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synthetic construct
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/mol_type="genomic DNA"
/db_xref="taxon:9826"
                                                                     /organism='Artificial
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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 ACH16833
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Abn22344 Human ORF
Aac06724 Human Ger
Ach16833 Human adu
Abl61825 Colon ade
Adn04087 Antipsori
Adp21384 Gene PLN
Ach16738 Human adu
Ach16738 Human adu
Ach17005 Human adu
Ach18023 Human adu
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Ach18065 Human adu
Ach18065 Human adu
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Ach16309 Human col
Abk83374 Human col
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. Aak28730 Human	Aba24770 Probe	Aba44562 Human	Aai34661 Probe	Aba55007 Human	Aail3308 Probe	Acf73801 Stap	Abt14895 Pati	Aax24906 Mouse	Acn44341 Moi	Adq79072 Novel	Aa141031 DNA	Aac85836 Nuc	Aac75801 Hum		Adq99406 DNA	Aai59183 Hum	Adq21778 Human sof	Aac77686 Humi	Aaz77530 Humi	Acn38837 Tur	Adr25399 Bro	Adf81412 Leu	Abk83658 Huma	Adc37617 Human nuc
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ALIGNMENTS

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RESULT 1
AAC64967
ID AAC6
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PR 15-A
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15-APR-1999;
01-JUN-1999;
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                                                                                                                                                                                                       Disclosure; Fig 11; 108pp; English.
                                                                                                                                                                                                                                                                                                              Identifying modulators of sarco/endoplasmic reticulum calcium ATPase, useful potentially for treating disorders of calcium homeostasis, e.g.
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99GB-00012736.
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BVO

The present invention is concerned with methods of using C. elegans identify compounds which are capable of up- and down-regulating the activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). protein is involved in cell signalling, and elevated levels affect cellular processes such as contraction, secretion and cell cycling.

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19-APR-2002;
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08-MAY-2002;
09-MAY-2002;
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09-MAY-2002;
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10-APR-2002;
10-APR-2002;
                                                                                          Mendrick
Elashoff
                            identifying profile of a
                                         Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene express:
                                                                                                                                                                09-JUL-2002;
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11-APR-2002;
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13-MAR-2002;
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                                                                     2003-731472/69.
                     values.
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2002US-0371413P
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2002US-0374139P
2002US-037853P
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2002US-0398665P
2002US-0394253P
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; 2002US-0363534P.
; 2002US-0370248P.
; 2002US-0371134P.
; 2002US-0371135P.
                                                                                                                                                                                                                                                                                                                                                                                                                     t; gene expression profile; heparker; toxicity progression; drug heparocyte toxicity modelling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 45
                                                                                                                                                                                                                                                                                                                                        2003WO-US003482.
                                                                                                                        21501
                                                                                                                                           2003US-0442900P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                   Porter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
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                              or cell sample
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Pred. No. 3.
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                             comprises comparing a gene expression to a database of Tox mean and non-Tox
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                                                                                                                                                                                                                                                                                                                                                                                                                       drug screening;
ing; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                           hepatotoxicity;
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                                                                      The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has present a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte or cell sample that sequence represents a primary rat hepatocyte or contents.
  Sequence
                                                        toxicity
                            screening. The present sequence from the present invention.
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184 A; 178 C; 141 G; 198
     T; 0 U;
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            TCTCATCTGCCTCCTGCTGATTTGCATTATCGTCATGCTCCTG 108
                                                             TGAGAGAAGGCCTCAGGCCAGGAAACCTCCAGAATGCTTTCATTGCTTTTGTCTGAT
 CTTGATATGTCTGCTGCTGATATGCATCATTGTGATGCTTCTG 329
                                            TGAAATGCCCCAGCAAGCGCGTCAGAACCTCCAGAACCTCTTTATCAATTTCTGTCTCAT 286
                                                                                        46.5%;
nilarity 68.0%;
Conservative
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                                                                                                      Score 50.2; DB 10 Pred. No. 8.1e-06;
                                                                                           Mismatches
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                                                                                           Indels
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                                                                                           Gaps
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RESULT 3
ADR97285
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                                                                                                               US2004191802-A1
                                                                                                                       Homo sapiens.
                                                                                                                                       Human phospholamban polymorphism fragment
                                                                                                                                human; phospholamban; polymorphism; cardiovascular disease.
                                                                                                                                                                standard; DNA; 159
                                                                                                                                                (first
                                                                                                                                                entry.
                                                                                                                                        DNA.
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Kranias 22-OCT-2003; 2003US-00691412 (HAGH/) KRAN/) EG, KRANIAS E G. HAGHIGHI K. Haghighi 2002US-0420295P 7

Phospholamban polymorphism assessment in individual, for determining for developing cardiovascular disease, by comparing analysis of the nucleotide fragment with a predetermined phospholamban nucleotide sequence risk

WPI; 2004-689841/67

Claim 15; SEQ ID NO 1; 15pp; English

The invention relates to a method of phospholamban polymorphism assessment in an individual which comprises comparing the analysis nucleotide fragment with a predetermined phospholamban nucleotide fragment to determine whether the individual carries a phospholamban polymorphism. The methods and phospholamban polymorphism. are useful for determining an the analysis polymorphism the

Claim 44; SEQ ID

NO 3624; 874pp; English

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Result
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Listing first 45 summaries
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9b est4:

9b est5:

9b est6:

9b gs1:

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                BG379827
AI603160
BF395370
BI296789
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3037.641 Million cell updates/sec
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2 MI-R-C2p

5 MI-R-B01-

7 MI-R-B01-

7 MI-R-C90-

1 MI-R-C90-

1 MI-R-C90-

2 MI-R-B01-

3 MI-R-B01-

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3 MI-R-B01-

3 MI-R-C90-

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7 BX923697
8 892817 MA
UI-R-BJ1-
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BX669692
LOCUS
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AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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JOURNAL
Query Match
                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adapt
at sigenasupport@jouy.inra.fr to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche
Chemin de Borde-Rouge - Auzeville
cedex, FRANCE
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08
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/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scac0028i.c.02"
                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
47.0%;
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CK357447	CK359188	CK357746	CK355453	CK355445	CK359219	CK356371	CK355314	CK357747	CK356439	CK357123	CK355359	CK357232	CK357243	CK356296	CK358464	CK359590	CK358482	AI103929	BF525010	BI290034
AGENCOURT	EST213218	UI-R-ABO-	UI-R-DKO-																	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 381)
Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S., Soares,M., Bonaldo,F. and Hatey,F. BX669692 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0028i.c.02 5prim, mRNA sequence. A Pig Normalised Multi-Tissue cDNA Library Unpublished (2003) /tissue type="mixed"
/clone Tib="Sus Scrofa library (scac)"
/clone Tib="Sus Scrofa library (scac)"
/note="Vector: pT7T3D-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, bypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder" adaptator and repetitions. Contact us obtain the chromatogram of this Agronomique BP27, 31326 mRNA linear Castanet-Tolosan Euteleostomi; Sus. EST 07-MAY-2004

Length 381;

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                                                                                                              66 TCTCATCTGCCTCCTGCTGATTTGCATTATCGTCATGCTCCT 107
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                                                                                                                                                                                                                                                                                              70;
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                                                                                                                                                                                                                                          6 TGAGAGAAGGCCTCAGGCCAGGAACCTCCAGAATGCTTTCATTGCTTTTTGTCTGAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetique Animale
Institut National de la Recherche
Chemin de Borde-Rouge - Auzeville
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1 (bases 1 to 702)

Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S., Soares, M., Bonaldo, F. and Hatey, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Pig Normalised Multi-Tissue cDNA Library Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BuS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Tosser-Klopp G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX922974.1 GI:41139822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                scan0013d.j.14 5prim, mRNA sequence.
                                                                                                                                                                                        TGAAATGCCTCAACAAGCACGTCAAAACCTTCAGAACCTATTTATCAATTTCTGTCTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scrofa (pig)
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                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="scan0013d.j.14"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/dev_stage="from embryos to squary
/clone_lib="Sus Scrofa library (scan)"
/clone_lib="Sus Scrofa library (scan)"
/clone_lib="Sus Scrofa library
/clone_lib-"sus scrofa library
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                                                                                                                                                                                                                                                                                                                       47.0%;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                    Score 50.8; DB 5;
Pred. No. 0.00013;
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                                                                                                                                                                                                                                                                                                                                             Length 702;
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                                                                                                                                                                                                                                                                  BX924154 Sus Scrofa library (scan) scan0011d.f.23 5prim, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 TGAGAGAAGGCCTCAGGCCAGGAAACCTCCAGAATGCTTTCATTGCTTTTTTGTCTGAT 65
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Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 724)
Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C.,
Soares, M., Bonaldo, F. and Hatey, F.
A Pig Normalised Multi-Tissue CDNA Library
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX674983 T24 bp mRNA linear EST 07-MAY-2004 BX674983 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0039i.h.23 5prim, mRNA sequence.
                                                                                                                                 Sus scrofa (pig)
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                        Bonnet, A.,
                                                    Mammalia; Eutheria;
1 (bases 1 to 740)
                                                                                                                                                                                                                    BX924154.1 GI:41141002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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  Soares, M.,
                                                                                                        Eukaryota; Metazoa;
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/db xref="taxon:9823"

/clone="scac0039i.h.23"

/tissue type="mixed"

/clone Tib="Sus Scrofa library (scac)"

/clone="vector: pT773D-pac vector; tissues: adipose tissue,
/norte="vector: pT773D-pac vector; tissues: heart,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo uretral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
  Tosser-Klopp, G., Benne, Bonaldo, F. and Hatey, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.0%;
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                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
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Cetartiodactyla; Suina; Suidae;
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EST 07-MAY-2004

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Gaps

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Maximum DB
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Perfect score:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/1.
2: /cgn2_6/ptodata/1.
3: /cgn2_6/ptodata/1.
4: /cgn2_6/ptodata/1.
5: /cgn2_6/ptodata/1.
6: /cgn2_6/ptodata/1.
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Gapop 10.0 , Gapext 1.0
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47.0
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/cgn2_6/ptcdata/1/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
/cgn2_6/ptcdata/1/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/1/ina/BTCTUS_COMB.seq:*
/cgn2_6/ptcdata/1/ina/backfiles1.seq:*
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US-09-949-016-15336
US-09-124-671-26
US-09-124-671-27
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Sequence 9, Appli
Sequence 13, Appl
Sequence 10799, A
Sequence 13181, A
Sequence 26, Appli
Sequence 1076, Appli
Sequence 15336, A
Sequence 15336, A
Sequence 203, Appli
Sequence 203, Appli
Sequence 204, Appli
Sequence 204, Appli
Sequence 205, Appli
Sequence 15578, Appli
Sequence 11, Appli
Sequence 17088, Appli
Sequence 17088, Appli
Sequence 17088, A
Sequence 17446, A
Sequence 17449, A
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RESULT 1 US-09-549-872B-9 Sequence 9, Ap Patent No. 654 GENERAL INFORM APPLICANT: Zw APPLICANT: Zw APPLICANT: G APPLICANT: G APPLICANT: G APPLICANT: G APPLICANT: G APPLICANT: G FILE REFERENC CURRENT FILING PRIOR APPLICA PRIOR FILING PRIOR FIL		C C	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 00 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	c 28
SULT 1 Sequence 9, Application US/095498 Sequence 9, Application US/095498 Sequence 9, Application US/095498 Sequence 9, Application US/095498 Sepelicant: Zwaal, Richard APPLICANT: Egeart, Thierry TITLE OF INVENTION: COMPOUND SCR FILE REFERENCE: D00590/70008 (JR CURRENT PILING DATE: 2000-04-15 PRIOR APPLICATION NUMBER: US 60 PRIOR FILING DATE: 1999-04-15 PRIOR FILING DATE: 1999-04-15 PRIOR APPLICATION NUMBER: US 60) PRIOR FILING DATE: 1999-06-01 RIOR SEQ ID NOS: 39 SOPTWARE: PatentIN Ver. 2.0 SEQ ID NO 9 SEQ ID NO 9 SEQ ID NO 9 SEQ ID NO 9		27.4 27.4 27.4 27.2		27. 27. 27. 44.	17.7.
B-9 Application US 6540996 6540996 ORMATION: Zwaal, Richard Groenen, Jose Bogaert, Thie BOGANTION: COMPO PELICATION NUMBER: LING DATE: 1999-0 ICATION NUMBER: NG DATE: 1999-0 SEQ ID NOS: 39 PatentIn Ver: 2		44400	4444	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	004
-872B-9 e 9, Application US/095 NO. 6540996 INFORMATION: INFORMATION: ANT: Zwaal, Richard ANT: Zwaal, Richard ANT: Bogaert, Thierry OF INVENTION: COMPOUND EFERENCE: D00590/70008 EFERENCE: D00590/70008 EFERENCE: D00590/70008 EFILING DATE: 1999-04-15 APPLICATION NUMBER: GB FILING DATE: 1999-04-15 APPLICATION NUMBER: GB FILING DATE: 1999-06-01 OF SEQ ID NOS: 39 RE: PatentIn Ver. 2.0 NO 90 H: 159		119153 213456 323820 7644 372	2628 8590 10300 38575	489 601 957 1117 1117 1851 2120	143776 144034 483
Application US/09549872B 540996 RMATION: Zwaal, Richard Groenen, Jose Bogaert, Thierry ROBERTION: LICATION NUMBER: US/09/549, LICATION NUMBER: US/09/549, LICATION NUMBER: GB 9908670.4 CATION NUMBER: GB 9908670.4 CATION NUMBER: US 60/129,59 GDATE: 1999-04-15 CATION NUMBER: GB 9912736.7 GG DATE: 1999-06-01 ATEN 1999-06-01 EQ ID NOS: 3 VatentIn Ver. 2.0	_	4 US-09- 4 US-09- 4 US-09- 4 US-09- 4 US-09-		1 US-1 1 US-1 2 US-1 3 US-1	
549872B SCREENING METHODS (JRV/RE) US/09/549,872B 4-14 9908670.4 9908670.4 5 60/129,596 5 9912736.7	ALIGNMENTS	US-09-949-016-12378 US-09-820-007-3 US-09-949-016-14139 US-09-949-016-17610 US-09-270-767-5510	US-09-774-528-27 US-09-949-016-5562 US-09-949-016-636 US-09-949-016-17304 US-09-949-016-17378	US-09-107-433-492 US-09-949-016-82861 US-08-309-1828-1 US-09-552-225A-11 US-09-552-225A-11 US-09-949-016-3036 US-09-149-476-160	US-09-949-001-29 US-09-949-001-35 US-09-583-110-2272
		Sequence 123'8, A Sequence 3, Appli Sequence 14139, A Sequence 17610, A Sequence 5510, Ap	556 636 173		e 29, 1 e 35, 1 e 2272,

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RESULT 2
US-09-549-872B-13
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9
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milarity 68.6%;
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Pred. No. 5.6e-08;
0; Mismatches 32
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US-09-949-016-1439; Sequence 1439; Application; Patent No. 6812339
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US-09-513-999C-10799
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PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR PILING DATE: 1999-04-15
PRIOR PPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
COMPANDE: DEFCATT VOT
                    GENERAL
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SOFTWARE: Patent.pm
SEQ ID NO 10799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6783961 GENERAL INFORMATION:
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LENGTH: 159
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10799,
                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                     LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
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Local Similarity 68.6%;
                   INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description of Artificial Sequence:HUMANIZED PLB cDNA
                                                                                                                                                                                                                                                                                      42.6%;
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Pred. No.
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Pred. No. 5.6e-08;
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; ORGANISM: Human
US-09-949-016-13181
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Matches
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SEQ ID NO 13181
LENGTH: 16062
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13181, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-09
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
NUMBER OF SEQ ID NOS: 207012
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 67; Conserv
                                                                                                                                                             12661 TGAAATGCCTCAACAAGCACGTCAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCAT 12720
12721 CTTAATATGTCTCTTGCTGATCTGTATCATCGTGATGCTTCT 12762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 CTTAATATGTCTCTTGCTGATCTGTATCATCGTGATGCTTCT
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                                              66 TCTCATCTGCCTCCTGATTTGCATTATCGTCATGCTCCT
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Pred. No. 1.7e-05;
0; Mismatches 35;
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Pred. No. 6.7e-06;
0; Mismatches 35
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OF DETECTION AND USES THEREOF
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US-09-124-671-26 ; Sequence 26, Application US/09124671A

RESULT 6

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 10
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM nucleic - nucleic search, using sw model
     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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108
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/ Ggn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USOA_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USOD_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USOD_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
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/ Cgn2_6/ptodata/1/pubpna/USOO_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/phbpna/USO7_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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46	50. 8	108	108	. 108		Score
42.6	47.0	100.0	100.0	100.0	100.0	Query Match Length DB ID
159	159	135	135	108	108	Length
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US-10-691-412-1	US-10-371-101-9	US-10-724-532-6	US-10-724-532-5	US-10-724-532-4	US-10-724-532-3	Query Query Match Length DB ID
Sequence 1, Appli	Sequence 9, Appli	Sequence 6, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 3, Appli	Description

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US-10-437-963-88641 US-10-292-798-1007 US-10-482-029-205 US-10-027-632-238890	-10-470-048B-40 09-864-761-3236 -10-767-795-147	-11-1 1	-10-023-21 -10-690-21 -10-425-11	09-925-301- -10-723-860 -10-037-270 -10-117-722	S-10-723-518-2 S-09-814-353-205 S-10-172-118-126 S-10-342-887-126 S-10-848-755A-14	-09-918-995 -10-815-514 -10-877-930 -10-873-594 -09-918-995 -09-918-995 -09-969-034	US-09-918-995-4045 US-09-873-367C-162 US-10-843-641A-162 US-09-918-995-3950 US-09-918-995-5235 US-09-918-995-4217
e 8864 e 1007 e 205, e 2388	e 40	e 25701, e 740, Ap 3, Appli 7, Appli	Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli Sequence 557, App Sequence 167740,	, e e 8 , 1 1 2 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	, , , , , , , , , , , , , , , , , , ,	5377, 26, Ag 26, Ag 26, Ag 3842, 17377, 4348,	Sequence 4045, Ap Sequence 162, App Sequence 162, App Sequence 3950, Ap Sequence 5235, Ap Sequence 4217, Ap

ALIGNMENTS

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TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo) plasmic FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
LENGTH 100
LENGTH 10
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US-10-724-532-3
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                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 108; DB 20; Best Local Similarity 100.0%; Pred. No. 1.3e-26; Matches 108; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: mus musculus
      61 CTGATTCTCATCTGCCTCCTGCTGATTTGCATTATCGTCATGCTCCTG 108
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; ORGANISM: mus musculus
US-10-724-532-5
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US-10-724-532-5
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; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4
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Publication No. US20040203027A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10724532 Publication No. US20040203027A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               SEQ ID NO 5
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CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILLING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR PILLING DATE: 2002-12-02
PRIOR FILING DATE: 2002-12-02
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TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                           ENGTH: 135
                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 100.0%; Score 108; DB 20; Local Similarity 100.0%; Pred. No. 1.3e-26;
                                                                                                                                                      108; Conservative
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73
                                    61 CTGATTCTCATCTGCCTCCTGCTGATTTGCATTATCGTCATGCTCCTG 108
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                                                                                                    1 ATGCATGAGAGAAAGGCCTCAGGCCAGAACCTCCAGAATGCTTTCATTGCTTTTTGT 60
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                                                                                                                                                      Score 108; DB 20;
Pred. No. 1.4e-26;
); Mismatches 0;
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RESULT 4

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APPLICANT: Zwaal, Richard
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035.US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT APPLICATION NUMBER: GB 9908670.4
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR PILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR PILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                      ; LENGTH: 159
; TYPE: DNA
; ORGANISM: SUS S
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; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6
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US-10-371-101-9
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PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/10724532
Publication No. US20040203027A1
                                                                                                                                                                        Matches
                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/10371101 Publication No. US20030149995A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 108; Conservative
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CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
114 CTTAATATGCCTCTTGCTGATTTGCATCATCGTGATGCTTCT
                      66 TCTCATCTGCCTGCTGATTTGCATTATCGTCATGCTCCT 107
                                                                                  54 TGAAATGCCTCAACAAGCACGTCAAAACCTTCAGAACCTATTTATCAATTTCTGTCTCAT 113
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                                                                                                                  6 TGAGAGAAGGCCTCAGGCCAGGCAGAACCTCCAGAATGCTTTTCATTGCTTTTTTTGTCTGAT
                                                                                                                                                                        Conservative
                                                                                                                                                                                         47.0%;
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                                                                                                                                                                     Score 50.8; DB 15
Pred. No. 3.8e-07;
0; Mismatches 32
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Scoring table:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: gb_ba:*
2: gb_htg
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5: gb_om
6: gb_ov
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12:
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Gapop 10.0 , Gapext 1.0
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108
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                                                     GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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SUMMARIES

c 19	c 18	c 17	c 16	15	C 14	c 13	c 12	c 11	c 10	o 9	ი 8	c 7	ი 6	ი 5	C 4	ი 3	ი 2	c 1	Result
47	47	47	47.6	50.2	50.2	50.2	50.2	50.2	50.2	50.8	50.8	50.8	50.8	50.8	50.8	50.8	52.4	52.4	Score
43.5	43.5	43.5	44.1	46.5	46.5	46.5	46.5	46.5	46.5	47.0	47.0	47.0	47.0	47.0	47.0	47.0	48.5	48.5	Query Match Length
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AC100317 Mus muscu	S46792 phospholamb	BC061097 Mus muscu	BX276081 Zebrafish	AC128365 Rattus no	AC097906 Rattus no	L03382 Rat phospho	X71068 R.norvegicu	S95849 Rattus sp.	S95853 phospholamb	X15075 Pig mRNA fo	AX040491 Sequence	AX040487 Sequence	AR302007 Sequence	AR302003 Sequence	BD247911 Method fo	BD247907 Method fo	Y00761 O.cuniculus	M63601 Rabbit phos	Description

ALIGNMENTS

ORIGIN	CDS	exon	m.RNA	source	FEATURES	PUBMED	JOURNAL	TITLE	AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS SEGMENT	VERSION	DEFINITION	RESULT 1 RABPHLAM2/c LOCUS
/ FINITE LONG PEQUATORY PROFEST OF BRICOPERSHIP CALATPRAGE (CAATPRAGE) / COGOON_SEATE=1 / COCOON_SEATE=1 /		/product="phospholamban" 428 858	/organism="Gryctolagus cuniculus" /mol_type="genomic DNA" /db_xref="taxon:9986" /tissue lib="rabbit genomic" join(M63600.1:855943,428858)	1 858	Location/Qualifiers	יייייייייייייייייייייייייייייייייייייי	J. Biol. Chem. 266 (18), 11669-11675 (1991)	structure of the rabbit phospholamban gene, cloning of the human	Fujii, J., Zarain-Herzberg, A., Willard, H.F., Tada, M. and	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Eutereoscomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. 1 (bases 1 to 858)		Oryctolagus cuniculus (rabbit)	phospholamban. 2 of 3	M63601.1 GI:165636	phospholamban gene, p	RABPHLAM2 858 bp DNA linear MAM 27-APR-1993

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REFERENCE
AUTHORS
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ORGANISM
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Matches 71
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 159)
                                                                 BD247907 159 bp
Method for screening compounds.
BD247907
BD247907.1 GI:33057677
JP 2002541859-A/9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
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Rabbit cardiac and slow-twitch muscle
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FEBS Lett. 227 (1),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lett.
                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="phospholamban"
/protein_id="CAA68730.1"
/db_xref="GI:1662"
/db_xref="GA:270006"
/db_xref="GA:270006"
/db_xref="GA:270006"
/translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryctolagus cuniculus"
/mol_type="mRNA"
/db_xref="taxon:9986"
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               Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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phospholamban.
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Pred. No. 2.2e-06;
0; Mismatches 31
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TITLE
JOURNAL
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TITLE
Query Match
Best Local Similarity
Matches 70; Conserv
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Method for screening compounds

Patent: JP 2002541859-A 9 10-DEC-2002;

DEVGEN NV
OS Sus sp. (pig)
PN JP 2002541859-A/9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 99127367.

PI TUN-1999 GB 99127367.
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT PC C1201/42, C12N15/09, C12Q1/02, C12N15/00
CC Method for screening compounds
FH Key
FT source

1. 159
FT source

/organism='Sus sp. (pig)'.
                                                                                                                                                                                                                                                                            Method for screening compounds
patent: JP 2002541859-A 13 10-DE
DEVGEN NV
OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PF 14-APR-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, PC C1201/42, C12N15/09, C12Q1/02
PC C12Q1/42, C12N15/09, C12Q1/02
PC C12Q1
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BD247911.1 GI:33057681
JP 2002541859-A/13.
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Zwaal,R., Groenen,J. and Bogaert,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic construct
synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other sequences;
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47.0%;
nilarity 68.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT C12Q1/42, C12N15/09, C12Q1/02, C12N15/00 Description of Artificial Sequence: HUMANIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:9826"
                                                                                                                                                                                                                                               /organism='Artificial
Location/Qualifiers
                                                                                                                                       organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             artificial sequences
; Score 50.8; Di
; Pred. No. 6e-0;
0; Mismatches
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                               8; DB 6e-06;
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2002as:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
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Match
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Gapop 10.0 , Gapext 1.0
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108
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Length
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(c) 1993 - 2005
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   \frac{1}{2}
                 ADB53082
ABN22344
AAC06724
AAC16833
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          Aac64967 Pig phosp
Adb53082 Primary r
Adr97785 Human pho
Abb22344 Human ORF
Aac06724 Human Gec
Ach16833 Human adu
Abl61825 Colon ade
Adn921184 Gene PDY
Adg21184 Gene PDY
Adg21185 Human adu
Ach16738 Human adu
Ach1705 Human adu
Ach1705 Human adu
Ach18653 Human adu
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Ach16630 Human adu
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Abg60653 Human CON
Abg60653 Human CON
Abg60653 Human CON
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4.5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	c 26	25	24	23	22	21
30	30	30	30	30	30	30.2	30.2	30.4	30.4	31.2	32	32	32	32	32	32	32.8		32.8		32.8	•	32.8	32.8
27.8	27.8	27.8	27.8	27.8	27.8	28.0	28.0			28.9	29.6	29.6		29.6				30.4	30.4			30.4		30.4
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Aak28730 Human bon	Aba24770 Probe #32	Aba44562 Human bre	Aai34661 Probe #33		Aai13308 Probe #32	Acf73801 Staphyloc	Abt14895 Pathogen	Aax24906 Mouse elo	Acn44341 Mouse mRN	Adq79072 Novel can	Aal41031 DNA encod	Aac85836 Nucleotid	Aac75801 Human ORF		Adq99406 DNA encod	Aai59183 Human pol	Adq21778 Human sof	Aac77686 Human can	Aaz77530 Human ova	Acn38837 Tumour-as	Adr25399 Breast ca	Adf81412 Leukaemia	Abk83658 Human cDN	Adc37617 Human nuc

AAC64967 standard;

CDNA;

159 ₿₽

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RESULT 1
AAC649867/c
ID CAC649
XX AAC649
XX AC649
XX Pig; B
XX Pig
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15-APR-1999;
01-JUN-1999;
                                                                                                                                                                                                                                                                                                     Identifying modulators of sarco/endoplasmic reticulum calcium ATPase, useful potentially for treating disorders of calcium homeostasis, e.g cardiac hypertrophy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pig; sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling;
cardiac hypertrophy; heart failure; hypertension; Darier-White disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-658082/64.
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99US-0129596P.
99GB-00012736.
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The present invention is concerned with methods of using C. elegans identify compounds which are capable of up- and down-regulating the activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). protein is involved in cell signalling, and elevated levels affect cellular processes such as contraction, secretion and cell cycling.

The This ő

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Disclosure; Fig 11; 108pp; English.

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Matches 70
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11-APR-2002
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13-MAR-2002;
08-APR-2002;
10-APR-2002;
                                                                                          Mendrick
Elashoff
                 mean
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                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypertension,
                           Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene express; profile of a tissue or cell sample to a database of Tox mean and non-
                                                                                                                                                                                                                                                                                                                                              04-FEB-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                              toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
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                                                                                                                         (GENE-)
                 values.
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                                                                                                                                                                                             2002US-0353171P.
2002US-03534P.
2002US-0370248P.
2002US-0371134P.
2002US-0371135P.
2002US-0371150P.
2002US-0371413P.
2002US-0371413P.
2002US-0373601P.
2002US-0373602P.
2002US-0378379P.
2002US-0378652P.
2002US-0378652P.
2002US-0378653P.
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2002US-0394230P.
2002US-0394253P.
2002US-0407688P.
2003US-0442900P.
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Pred. No. 3
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                            comprises comparing a gene expression to a database of Tox mean and non-Tox
                                                                                                   Higgs
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-:
                                                                                                    Castle
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Claim 44; SEQ ID

NO 3624; 874pp; English

The invention relates to a method of phospholamban polymorphism assessment in an individual which comprises comparing the analysis nucleotide fragment with a predetermined phospholamban nucleotide fragment sequence to determine whether the individual carries a phospholamban polymorphism. The methods and phospholamban polymorphism.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                             Phospholamban polymorphism assessment in individual, for determining for developing cardiovascular disease, by comparing analysis of the nucleotide fragment with a predetermined phospholamban nucleotide
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ORIGIN RESULT 1 BX669692/c FEATURES COMMENT REFERENCE SOURCE ORGANISM DEFINITION KEYWORDS ACCESSION VERSION TITLE JOURNAL AUTHORS source Unpublished (4000)
Contact: Tosser-Klopp G
Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Institut National de la Recherche BP27, 31326 Castanet-Tolosan Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 381)
Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S., Soares,M., Bonaldo,F. and Hatey,F. Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this A Pig Normalised Multi-Tissue cDNA Library Unpublished (2003) Sus scrofa (pig) Sus scrofa BX669692 BX669692 Sus Scrofa library Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08 BX669692.1 GI:37979481 scac0028i.c.02 5prim, mRNA sequence. /organisma="Sus scrofa"
//organisma="Sus scrofa"
//db xref="taxon:9823"
//db xref="taxon:9823"
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Query Match

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Score 50.8;

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Length 381;

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Fax: 33 (0) 5.61.28.53.08
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Contact: Tosser-Klopp G Genetique Animale
Institut National de la Recherche Agronomic Chemin de Borde-Rouge - Auzeville BP27, 31:
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BX922974.1 GI:41139822
EST:
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Soares, M., Bonaldo, F. and Hatey, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 702)
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                                                                                   AGAAGCATCACGATGATGCAAATCAGCAAGAGGCATATTAAGATGAGACAGAAATTGATA
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/clone="scan0013d.;14"
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/dev stage="from embryos to scan)"
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/clone_tibs="sus scrofa library brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo uretral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Sus scrofa"
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Location/Qualifiers
                                                                                                                                                                       47.0%;
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Pred.
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                                                                                                                                                                         50.8; DB 5;
No. 0.00013;
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BP27, 31326
                                                                                                                                                          32;
                                                                                                                                                                                          Length 702;
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REFERENCE
                                                                                                                                                            DEFINITION
                                                                                                                         ACCESSION
                                                                                       KEYWORDS
                                                                                                          VERSION
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RESULT 3

Bonnet, A., Soares, M.,

Tosser-Klopp,G., Benne,F., Bonaldo,F. and Hatey,F.

Cabau, C.,

Euteleostomi; Sus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 740)

Sus scrofa (pig)

BX924154.1 GI:41141002

BX924154

BX924154 Sus Scrofa library (scan) S scan0011d.f.23 5prim, mRNA sequence.

740 bp

mRNA

Sus scrofa cDNA clone

EST 07-MAY-2004

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Matches
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  278
                                              62
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Soares,M., Bonaldo,F. and Hatey,F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
                                                                                                             2 AGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAAATCAGACAAAAAGCAATG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: toser@foulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemin de Borde-Rouge cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tosser-Klopp G
Genetique Animale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 724)
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                                                                                                                                                                                                     Similarity
                                            AAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA 103
AATAGGTTCTGAAGGTTTTGACGTGCTTGTTGAGGCATTTCA
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0039,
                                                                                                                                                                                                                                                                                    /db_xref="taxon:9823"
/clone="scac0039i.h.23"
/clone="scac0039i.h.23"
/clone="scac0039i.h.23"
/clone=Tib="Sus Scrofa library (scac)"
/clone=Tib="Sus Scrofa library (scac)"
/clone=Tib="Sus Scrofa library (scac)"
/note="Vector: pT/73D-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"
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                                                                                                                                                                                                     Score 50.8; DB 5; Pred. No. 0.00013;
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Auzeville
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BP27, 31326
                                                                                                                                                                                                                          Length 724;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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caggagcatgacgataatgc.....tgaggccttctctcatgcat
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Length
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                 US-09-549-872B-9
US-09-549-872B-13
US-09-543-99C-1079
US-09-949-016-1439
US-09-949-016-13181
US-09-949-016-15336
US-09-949-016-15336
US-09-949-016-15336
US-09-949-016-15336
US-09-188-930-203
US-09-949-016-17688
US-09-949-016-17088
US-09-949-016-17449
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             Sequence 9, Appli
Sequence 13, Appl
Sequence 10799, Ap
Sequence 1139, Ap
Sequence 26, Appl
Sequence 1076, Ap
Sequence 1076, Ap
Sequence 1161, Appl
Sequence 203, Appl
Sequence 203, Appl
Sequence 203, Appl
Sequence 5041, Appl
Sequence 511, Appl
Sequence 11, Appl
Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                   RESULT 2
US-09-549-872B-13/c
US-09-549-872B-13/c
Sequence 13, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
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APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
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25.0	25.2	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.6	25.6
372	7644	323820	213456	119153	38575	_					1117		601	489	483	144034	143776
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US-09-270-767-5510	US-09-949-016-17610	US-09-949-016-14139	US-09-820-007-3	US-09-949-016-12378	US-09-949-016-17304	US-09-949-016-636	US-09-949-016-5562	US-09-774-528-27	US-09-149-476-160	US-09-949-016-3036	US-09-552-225A-11	US-08-309-182B-1	US-09-949-016-82861	US-09-107-433-492	US-09-583-110-2272	US-09-949-001-35	US-09-949-001-29
	Seguence 17610, A	Sequence 14139, A	Sequence 3, Appli	Sequence 12378,	Sequence 17304,	Sequence 636, App	Sequence 5562, Ap	Sequence 27, Appl	Sequence 160, App	Sequence 3036, Ap	Sequence 11, Appl	Sequence 1, Appli	Sequence 82861,	Sequence 492, App	Sequence 2272, Ap	Sequence 35, Appl	•

ALIGNMENTS

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APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILLS REFERENCE: D00590/70008 (JRV/RE)
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US/09/549,8728
CURRENT FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR SEQ ID NOS: 39
SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9
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; Sequence 9, Application US/09549872B
; Patent No. 6540996
                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 70; Conserv
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                                                                                                       155 AGAAGCATCACGATGATGCAAATCAGCAAGAGGCATATTAAGATGAGACAGAAATTGATA
95
                                62 AAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA 103
                                                                                                                                                                  N
                                                                                                                                             AGGAGCATGACGATAATGCAAATCAGCAGGAGGAGGATGAGAATCAGACAAAAAGCAATG
AATAGGTTCTGAAGGTTTTGACGTGCTTGTTGAGGCATTTCA
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Pred. No. 5.6e-08;
0; Mismatches 32
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0;

Gaps

96 61

CURRENT FILING DATE:

2000-04-14

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PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
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               US-09-949-016-1439/c
Sequence 1439, Application
Patent NO. 6812339
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-10799
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SOFTWARE: Patent.pm
SEQ ID NO 10799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Ductert, A.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10799, Application US/09513999C Patent No. 6783961
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 APPLICANT:
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION:
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Local Similarity 68.6%;
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 VENTER, J.
                                                                                                                                   AATAGATTCTGTÄGCTTTTGACGTGCTTGTTGAGGCATTTCA
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                                                                                                                                                                                                                                                                                  42.6%;
Craig et al
                                                   US/09949016
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                                                                                                                                                                                                                                                                                  Score 46;
Pred. No.
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Thes 35; Indels
                                                                                                                                                                                                                                                                                                 DB 4;
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                                                                                                                                                                                                                                                                                                   Length 480;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 13181
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LENGTH: 1635
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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67; Conserv
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AATAGATTCTGTAGCTTTTGACGTGCTTGTTGAGGCATTTCA
                                            AAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA 103
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                                                                                                                                                                                          42.6%;
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Pred. No. 1.7e-05;
0; Mismatches 35
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RESULT 6 US-09-124-671-26/c ; Sequence 26, Application US/09124671A

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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seq length: 2000000000
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1: /cgn2_6/ptcdata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptcdata/1/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2_6/ptcdata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2_6/ptcdata/1/pubpna/USO6_NEW_PUB.seq:*

5: /cgn2_6/ptcdata/1/pubpna/USO6_PUBCOMB.seq:*

6: /cgn2_6/ptcdata/1/pubpna/USO7_NEW_PUB.seq:*

7: /cgn2_6/ptcdata/1/pubpna/USO7_PUBCOMB.seq:*

8: /cgn2_6/ptcdata/1/pubpna/USO7_PUBCOMB.seq:*

9: /cgn2_6/ptcdata/1/pubpna/USO9_PUBCOMB.seq:*

10: /cgn2_6/ptcdata/1/pubpna/USO9_PUBCOMB.seq:*

11: /cgn2_6/ptcdata/1/pubpna/USO9_PUBCOMB.seq:*

12: /cgn2_6/ptcdata/1/pubpna/USO9_PUBCOMB.seq:*

13: /cgn2_6/ptcdata/1/pubpna/USO0_PUBCOMB.seq:*

14: /cgn2_6/ptcdata/1/pubpna/USO0_PUBCOMB.seq:*

15: /cgn2_6/ptcdata/1/pubpna/USO0_PUBCOMB.seq:*

16: /cgn2_6/ptcdata/1/pubpna/USO0_PUBCOMB.seq:*

16: /cgn2_6/ptcdata/1/pubpna/USO0_PUBCOMB.seq:*

17: /cgn2_6/ptcdata/1/pubpna/USOO_PUBCOMB.seq:*

18: /cgn2_6/ptcdata/1/pubpna/USOO_PUBCOMB.seq:*

20: /cgn2_6/ptcdata/1/pubpna/USOO_PUBCOMB.seq:*

21: /cgn2_6/ptcdata/1/pubpna/USOO_PUBCOMB.seq:*

22: /cgn2_6/ptcdata/1/pubpna/USOO_PUBCOMB.seq:*

23: /cgn2_6/ptcdata/1/pubpna/USOO_PUBCOMB.seq:*

24: /cgn2_6/ptcdata/1/pubpna/USOO_PUBCOMB.seq:*

25: /cgn2_6/ptcdata/1/pubpna/USOO_PUBCOMB.seq:*

26: /cgn2_6/ptcdata/1/pubpna/USOO_PUBCOMB.seq:*
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Match Length DB
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          155220
  US-10-724-532-3

US-10-724-532-4

US-10-724-532-6

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US-10-371-101-9

US-10-371-101-13

US-10-691-412-1
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Sequence 3, Appli
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Sequence 6, Appli
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Sequence 1, Appli
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13	21	17	19	19	9	21	v	ø	13	19	20	18	21	14	9	17	15	20	9	21	18	17	10	21	H	10	10	21	20	20	10	10	10	10	21	10	10
US-10-027-632-238890	82-02	-10-292-798-1007	-10-437-963-	-10-767-795-147	9-864-761-3	-10-470-048E	٢	09-994-48	10-087-192-7	US-10-767-701-25701	10-425-115-1	10-425-114-55	US-10-690-276-3	-10-023-219-	9-7:	17-722-107	10-037-270-107	-10-723-860-459	09-925-301-80	-10-848-755A-14	-342-887-1	-10-172-118-126	-09-814-353-	0-723	-09-969-034-43	-09-918-995-173	-09-918-995-3	-10-873-594-2	-10-877-930-2	-10-815-514-2	-918-995-537	-09-918-995-421	-09-918-995-523	-09-918-995-395	-10-843-641A-	-09-873-367C-16	US-09-918-995-4045
e 238	Seguence 205, App	e 100	e 886	e 147!	3236	e 40,	7, A	3, Appli	e 74(equence 2	equence 1	ر.	w	'n	5, Appl	μ.	equence 1076,	e 4598	m	e 148,	e 1260	1260	2050	2, A	4348,	e 1737	3842	e 26,	e 26,	e 26,	e 53	e 4217	e 5235	e 3950		162,	3

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; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
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US-10-724-532-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10724532
Publication No. US20040203027A1
GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
                                                                                                                                                      Query Match 100.0%; Score 108; DB 20; Best Local Similarity 100.0%; Pred. No. 1.3e-26; Matches 108; Conservative 0; Mismatches 0;
                                                      108
  61 GAAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCATGCAT 108
                                                                               1 CAGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAATCAGACAAAAAGCAAT 60
                                                      CAGGAGCATGACGATAATGCAAAATCAGCAGGAGGCAGATGAGAATCAGACAAAAAAGCAAT 49
                                                                                                                                                           Indels
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 108
TYPE: DNA
ORGANISM: mus musculus
US-10-724-532-4
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US-10-724-532-4
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Publication No. US20040203027A1

GENERAL INFORMATION:

APPLICANT: Reed, Thomas D

TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo) plasmic TITLE REFERENCE: SR RPA CURRENT APPLICATION NUMBER: US/10/724,532

CURRENT FILING DATE: 2003-11-29

PRIOR APPLICATION NUMBER: US 60/430322

PRIOR FILING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 135
TYPE: DNA
ORGANISM: mus musculus
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Best Local Similarity
                                                                                                                                                Matches 108;
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                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                   Query Match
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100.0%; Pred. No. 1.4e-26;
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APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
APPLICANT: Bogaert, Thierry
APPLICATION: COMPOUND SCREENING METH
FILE OF INVENTION: COMPOUND SCREENING METH
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: GB 9912736.7
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US-10-371-101-9/c
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Publication No. US20040203027A1

GENERAL INFORMATION:
APPLICANT: Reed, Thomas D

TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic TITLE OF INVENTION: Reticulum FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532

CURRENT APPLICATION NUMBER: US 60/430322

PRIOR APPLICATION NUMBER: US 60/430322

PRIOR APPLICATION NUMBER: US 60/430322

PRIOR FILING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.2
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Best Local Similarity 100.0%;
Matches 108; Conservative 0
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PRIOR APPLICATION NUMBER: 09/549,872
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                                                                          LENGTH: 159
TYPE: DNA
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BD030469 Sequence
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CQ718671 Sequence
AX329653 Sequence
M63603 Human phosp
BC005269 Homo Bapi
AL1355356 Homo Bapi
AL135536 Homo Bapi
AL1365974 Homo Bapi
AL13612 Canis fam
M16012 Canis fam
M16012 Canis card
M15393 Dog cardiac
Y00399 Dog phospho
AR121629 Sequence

AL031736 Human DNA AC116417 Mus muscu AC145916 Gallus ga CQ719769 Sequence

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       AX040491 Sequence
X15075 Pig mRNA fo
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X71068 R.norvegicu
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AC128365 Rattus no
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BX537355 Zebrafish
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Structure of the rabbit phospholamban gene, cDNA, and assignment of the gene to human c.
J. Biol. Chem. 266 (18), 11669-11675 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                      Original source text: Rabbit DNA
Location/Qualifiers
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            /translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL
|CIIVMLL"
                                                                                           /function="regulatory
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/db_xref="taxon:9986"
/tissue_lib="rabbit_genomic"
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product="phospholamban"
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Fujii, J., Lytton, J., Tada, M. and MacLennan, D.H.
Rabbit cardiac and slow-twitch muscle express the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phospholamban gene FEBS Lett. 227 (1),
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71; Conservative
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/db_xref="taxon:9986"
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/db_xref="UniProt/Swiss-Prot:P20006"
/translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL
                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="phospholamban"
/protein_id="CAA68730.1"
/protein_id="CAA68730.1"
/db_xref="GI:1662"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Oryctolagus"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                  GI:33057677
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               Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                         159 bp compounds.
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phospholamban.
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Pred. No. 1.1e-05;
0; Mismatches 31;
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Pred. No. 1.3e-05;
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                 Euteleostomi;
Sus.
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SOURCE
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TITLE
JOURNAL
Query Match
Best Local Similarity
Matches 70; Conserv
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OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PF 15-APR-1999 GB 9908670.4,15-APR-1999 US 60
PN 15-APR-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C1201/42,C12N15/09,C12Q1/02,C12N15/00
CC Description of Artificial Sequence:HUMANIZED PIC
Key Location/Qualifiers
FT source /organism='Artificial Sequence'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zwaal,R., Groenen,J. and Bogaert,T.

Method for screening compounds
Patent: JP 2002541859-A 9 10-DEC-2002;
DEVGEN NV
OS Sus sp. (pig)
PN JP 2002541859-A)9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PF 14-APR-2000 JP 2000612503
PF 14-APR-1999 GB 99.08670.4,15-APR-1999 GB 9912736.7
PI RICHARD ZWAAL,JOSE GROENEN,THIERRY PC C1201/42,C12N15/09,C1201/02,C12N15/
CC Method for screening compounds
FH Key Location/Qualifiers
FT source 1.159
FT source 1.159
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BD247911.1 GI:33057681
JP 2002541859-A/13.
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37.6%;
milarity 68.6%;
Conservative
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15-APR-1999 GB 9908670.4,15-APR-1999 US
NN-1999 GB 9912736.7
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0; Mismatches 32;
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   Score 50.8; DB 6;
Pred. No. 3.1e-05;
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Perfect score:
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1: geneseqn1900s:*
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         ABN22344
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        Aac64967 Pig phosp
Adb53082 Primary r
Adr97285 Human pho
Abn22344 Human ORF
Aac06724 Human Gec
Ach16933 Human adu
Abl61825 Colon ade
Adh021344 Gene Plvi
Adp21344 Gene Plvi
Adp21344 Gene Plvi
Ach16738 Human adu
Ach16738 Human adu
Ach17005 Human adu
Ach18023 Human adu
Ach18023 Human adu
Ach18049 KDEL rece
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Aac50498 KJEL rece
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22.8	22.8	22.8	22.8	22.8	22.8	23.1	23.1	23.3	23.3			24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	ė	25.9	25.9	
415	415	415	415	415	415	2229	473	2175	1938	13306	3925	3748	3708	3647	3647	3647	3647	2422	2419	1896	652	10625	10625	6536	
4	4	4	4	4	4	σ	13	N	1	10	12	w	N	13	13	10	σ	10	v	12	σ	σ	v	w	
AAK28730	ABA24770	ABA44562	AAI34661	ABA55007	AAI13308	ABK74380	ADQ79072	AAX24906	ACN44341	ADC86554	ADQ21778	AAC77686	AAZ77530	ACN38837	ADR25399	ADF81412	ABK83658	ADC37617	ADL62294	ADP07907	ABQ60653	AAL41031	AAC85836	AAC75801	
Aak28730 Human bon	Aba24770 Probe #32	Aba44562 Human bre	Aai34661 Probe #33	Aba55007 Human foe	Aai13308 Probe #32	Abk74380 Bacillus	Adq79072 Novel can	Aax24906 Mouse elo	Acn44341 Mouse mRN	Adc86554 Human GPC	Adq21778 Human sof	Aac77686 Human can	Aaz77530 Human ova	Acn38837 Tumour-as	Adr25399 Breast ca	Adf81412 Leukaemia	Abk83658 Human cDN	Adc37617 Human nuc	Adl62294 Human ova	Adp07907 Human RAD	Abg60653 Human col			Aac75801 Human ORF	

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RESULT 1
AAC64967
ID AAC6
15-APR-1999;
15-APR-1999;
01-JUN-1999;
                                                                                                                                                                                                        Pig; sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling; cardiac hypertrophy; heart failure; hypertension; Darier-White disease; Brodys disease; diabetes; ss.
                                                                                                                                                                               GB2349217-A.
                                                                                                                                                                                                                                      Pig phospholamban cDNA.
                                                                                            Zwaal R,
                                                                                                                                                    14-APR-2000; 2000GB-00009363.
                                                                                                                                                                                            Sus scrofa.
                                                                                                                                                                                                                                                    09-FEB-2001
                                                                                                                                                                                                                                                                 AAC64967;
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                                                                                                           (DEVG-) DEVGEN NV
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99US-0129596P.
99GB-00012736.
                                                                                                                                                                                                                                                                               CDNA; 159
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The present invention is concerned with methods of using C. elegans identify compounds which are capable of up- and down-regulating the activity of the sacro/endoplasmic reticulum calcium ATPase (SERCA). protein is involved in cell signalling, and elevated levels affect cellular processes such as contraction, secretion and cell cycling.

This The

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Identifying modulators of sarco/endoplasmic reticulum calcium ATPase, useful potentially for treating disorders of calcium homeostasis, e.g. cardiac hypertrophy.

WPI;

2000-658082/64. Groenen J,

Bogaert

Disclosure; Fig 11; 108pp; English.

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RESULT 2
ADB53082
ID B53082
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XX ADB5
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Best Local
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13-MAR-2002;
08-APR-2002;
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10-APR-2002;
                                                                                                                                                                                             Mendrick
Elashoff
                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
                                                             Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                                                                                                                                                                                                                                                  09-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypertension,
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                                             values.
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2002US-0373602P.
2002US-037810P.
2002US-0378370P.
2002US-0378653P.
2002US-0378653P.
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2002US-0394253P.
2002US-0407688P.
2003US-0442900P.
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Pred. No. 6.9e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic marker;
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Claim 44;

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NO 3624; 874pp; English

The invention relates to a method of phospholamban polymorphism assessment in an individual which comprises comparing the analysis nucleotide fragment with a predetermined phospholamban nucleotide fragment sequence to determine whether the individual carries a phospholamban polymorphism. The methods and phospholamban polymorphism of the individual carries a phospholamban polymorphism. The methods and phospholamban polymorphism of the individual is at risk for fragment are useful for determining if an individual is at risk for

phospholamban polymorphism ndividual is at risk for

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        effect, particularly hepatotoxicity, or a continuous genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocytoxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The
                                                                                                                                          Phospholamban polymorphism assessment in individual, for determining for developing cardiovascular disease, by comparing analysis of the nucleotide fragment with a predetermined phospholamban nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human phospholamban polymorphism fragment DNA.
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                                                                                                                                fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; phospholamban; polymorphism; cardiovascular disease.
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                                                                                                                              sequence.
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nilarity 68.0%;
Conservative
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Pred. No. 1.7e-05
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Listing first 45 summaries
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gb_est4::
gb_est5::
gb_est6::
gb_gs81::
gb_gs82:
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gb_est2:*
gb_htc:*
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 GenCore version (c) 1993 - 2005
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           CR471116
BG379827
AI603160
BF395370
BI296789
BE112568
BF395607
BF395607
                                                                                                            AI322542
BE115006
BF394968
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BI288911
BE099930
BF525258
                                                                                                                                                                                                               BX674983
BX924154
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BX922974
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BF547322 UI-R-C2p-
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BF394968 UI-R-CM0-
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BX922974 BX922974
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                                    7 UI-R-CSO-
0 UI-R-AEO-
0 UI-R-CMO-
9 UI-R-DKO-
8 UI-R-BJ1-
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1 UI-R-CS08
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CK357447	CK359188	CK357746	CK355453	CK355445	CK359219	CK356371	CK355314	CK357747	CK356439	CK357123	CK355359	CK357232	CK357243	CK356296	CK358464	CK359590	CK358482	AI103929	BF525010	BI290034	
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REFERENCE AUTHORS ACCESSION VERSION KEYWORDS RESULT 1
BX669692
LOCUS
DEFINITION SOURCE ORGANISM ORIGIN COMMENT FEATURES BTITLE **Bource** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 381)
Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Vill soares,M., Bonaldo,F. and Hatey,F.
A Pig Normalised Multi-Tissue cDNA Library Unpublished (2003)
Contact: Tosser-Klopp G Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan cedex, FRANCE Tel: 33 (0) 5.61.28.51.14

Tel: 33 (0) 5.61.28.53.08

Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this Concact. Concact Conca BX669692 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0028i.c.02 5prim, mRNA sequence. Sus scrofa Sus scrofa (pig) BX669692.1 GI:37979481 BX669692 /mol type="mRNA"

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Query Match

37.6%;

Score 50.8;

DB 5;

Length 381;

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RESULT 2
BX922974
LOCUS
  RESULT 3
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                                                                                                                                                                                                                                70;
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 702)

Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S., Soares,M., Bonaldo,F. and Hatey,F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08
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Chemin de Borde-Rouge - Auzeville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrota
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muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo uretral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"
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db_xref="taxon:9823"
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0; Mismatches 32
                                                                                                                                                                                                                              Score 50.8; DB 5; Pred. No. 0.00033; 0; Mismatches 32
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BP27, 31326 Castanet-Tolosan
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Sus scrofa
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
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Institut National de la Recherche
Chemi de Borde-Rouge - Auzeville
Cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
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Soares,M., Bonaldo,F. and Hatey,F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
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Sus scrofa
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BX674983 Sus Scrofa library (scac) Sus scrofa cDNA clone
scac0039i.h.23 5prim, mRNA sequence.
BX674983
  Bonnet, A.,
Soares, M.,
                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 724)
                                        1 (bases 1 to 740)
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pituitary gland, seminal vesicle, small intestine,
terus, adrenals, bulbo uretral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"
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Tosser-Klopp, G., Benne, Bonaldo, F. and Hatey, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.6%;
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                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50.8; DB 5; Pred. No. 0.00033; 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  column:
                                                                                                                                                                                                                                                     740 bp
                       Benne, F.,
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BP27, 31326
                                                                                                                                                                                                                                  mRNA linear EST
Sus scrofa cDNA clone
                         Cabau, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 724;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                       Score
  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                       Query
Match
                                                                                                                                                                                                                                                                                                                                                        Issued_Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1202784 segs, 818138359 residues
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  37.6
37.6
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 7, 2005, 09:02:25; Search time 77.2222 Seconds (without alignments) 2860.541 Million cell updates/sec
                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                       DB
          US-09-549-872B-9
US-09-513-990C-10799
US-09-913-990C-10799
US-09-949-016-13181
US-09-949-016-13181
US-09-949-016-13588
US-09-912-540-1172
US-09-949-016-15336
US-09-949-016-15336
US-09-949-016-15336
US-09-949-016-2378
US-09-949-016-1304
US-09-949-016-1308
US-09-949-016-12378
US-09-949-016-12378
US-09-949-016-12378
US-09-949-016-12378
US-09-949-016-12378
US-09-949-016-12378
US-09-949-016-12378
US-09-949-016-12378
US-09-949-016-236
US-09-949-016-2378
US-09-949-016-2378
US-09-949-016-238
                                                                                                                                                                                                                                                                                                   SUMMARIES
 Sequence
                                                                                                                                                                                                                                                                       Description
9, Appli
13, Appl
1439, Ap
1439, Ap
26, Appl
13181, A
26, Appl
3, Appli
3, Appli
1172, Ap
1172, Ap
1174, Ap
1536, Ap
1536, App
636, App
636, App
636, App
14880, A
14880, A
12378, Ap
12378, Ap
12378, App
1203, App
203, App
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US-09-489-039A-5041

US-09-949-016-200644

US-09-949-016-16824

US-09-949-016-17086

US-09-949-016-17390

US-09-949-016-17391

US-09-949-016-17391

US-09-949-016-17391

US-09-949-016-15578

US-09-949-016-15578

US-09-949-016-15578

US-08-916-171E-999

US-08-916-171E-999

US-08-916-171E-999

US-08-916-171E-999

US-08-916-171E-999

US-08-916-171E-999

US-08-916-346-5

US-09-349-016-3036

US-09-949-016-3036

US-09-949-016-3036
Sequence 5041, Ap
Sequence 200644,
Sequence 200790,
Sequence 16824, A
Sequence 17306, A
Sequence 17391, A
Sequence 17391, A
Sequence 1, Appli
Sequence 1929, App
Sequence 15578, A
Sequence 15578, A
Sequence 999, App
Sequence 999, App
Sequence 5, Appli
Sequence 5, Appli
Sequence 3036, App
Sequence 160, App
Sequence 10, App
Sequence 10, Appli
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RESULT 1 US-09-549-872B-9

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RESULT 2
US-09-549-872B-13
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9
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Best Local S
Matches 70
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                                                                                                                                                                                                                                                                                 114 CTTAATATGCCTCTTGCTGATTTGCATCATCGTGATGCTTCT 155
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Conservative
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0;

Gaps

113

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US-09-949-016-1439
Sequence 1439, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
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                                                                                          RESULT 4
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; ORGANISM: Homo sapiens
US-09-513-999C-10799
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PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961
FILE REFERENCE: 59 US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10799
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Best Local S
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Best Local S
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LENGTH: 159
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Description of Artificial Sequence:HUWANIZED OTHER INFORMATION: PLB cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 480
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67; Conserv
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                                                                                                                                                                                                                                                                                              Conservative
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65.7%;
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Pred. No. 8.4e-
0; Mismatches
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Pred. No. 1.2e-07;
0; Mismatches 32;
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ches 35; Indels
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                                                                                                                                                                                                                                                        ; ORGANISM: Human
US-09-949-016-13181
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US-09-949-016-13181
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                                                                                                                                                           Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1439
                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13181
LENGTH: 16062
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Best Local
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-9-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILLING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Human
                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1635
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les 67; Conserv
                                                                                  12661 TGANATGCCTCAACAAGCACGTCAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCAT 12720
12721 CTTAATATGTCTCTTGCTGATCTGTATCATCGTGATGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 CTTAATATGTCTCTTGCTGATCTGTATCATCGTGATGCTTCT 336
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                        TCTCATCTGCCTGCTGATTTGCATTATCGTCATGCTCCT 119
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Pred. No. 4.2e-05;
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Pred. No. 1.5e-05;
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OF DETECTION
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RESULT 6 US-09-124-671-26

Sequence

26, Application US/09124671A

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                           Score
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications NA:*

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*

6: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*

13: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

20: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

21: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

22: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

23: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

24: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

25: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

26: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
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Match Length DB
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     US-10-724-532-5

US-10-724-532-6

US-10-724-532-3

US-10-724-532-4

US-10-371-101-9

US-10-371-101-19

US-10-691-412-1
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Sequence 5, Appli
Sequence 6, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 13, Appli
Sequence 13, Appli
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16	US-09-974-300-	229	•	۳		_
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80, A	US-09-9	80	24.9	ü		_
e 148,	US-10-848-755	7	•	۳		_
e 12	US-10-342-887-	7	•	'n		_
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equence 3,	US-10-023-219-	u	٠	35		_
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e 26,	US-10-877-930-2		•	4.	16	
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e 4217	US-09-918-995-421	4	•	4.	13	
e 5235	US-09-918-995-52	œ	٠		12	
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equence 162,	US-10-843-641A-16	1635	•	46	10	
e 162,	US-09-873-367C-16	635	•	46	9	
Sequence 4045, Ap	US-09-918-995-404	u	•	46	œ	

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; ORGANISM: mus musculus
US-10-724-532-5
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US-10-724-532-5
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo) plasmic TITLE OF INVENTION: Reticulum FILE REFERENCE: SR RPA CURRENT APPLICATION NUMBER: US/10/724,532 CURRENT FILING DATE: 2003-11-29 PRIOR APPLICATION NUMBER: US 60/430322 PRIOR APPLICATION NUMBER: US 60/430322 PRIOR FILING DATE: 2002-12-02 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin version 3.2 SEQ ID NO 5 LENGTH: 135 LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/10724532
Publication No. US20040203027A1
GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
                                                                                                                                                    Query Match 100.0%; Score 135; DB 20; Best Local Similarity 100.0%; Pred. No. 7.7e-36; Matches 135; Conservative 0; Mismatches 0;
  61 ATTGCTTTTTGTCTGATTCTCATCTGCCTCCTGCTGATTTGCATTATCGTCATGCTCCTG 120
                                                                                1 GAGAGAAAGCTTATGCATGAGAGAAGGCCTCAGGCCAGGAACCTCCAGAATGCTTTC 60
                                                     GAGAGAAAGCTTATGCATGAGAGAAGGCCTCAGGCCAGGCAGAACCTCCAGAATGCTTTC
                                                                                                                                                         Indels
                                                                                                                                                                                                     Length 135;
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                                                                                                                                                         Gaps
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FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 135
TYPE: DNA
ORGANISM: mus musculus
US-10-724-532-6
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                                                                                                                                      ; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-3
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US-10-724-532-3
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US-10-724-532-6/c
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APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR FILING DATE: 2002-12-02
PRIOR FILING DATE: 2002-12-02
PRIOR FILING DATE: 2002-12-02
PRIOR FILING DATE: 2002-13-03
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APPLICANT: Reed, Thomas D

TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic

TITLE OF INVENTION: Reticulum
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Publication No. US20040203027A1
                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.2 SEQ ID NO 3
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Publication No. US20040203027A1
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Best Local Similarity
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Best Local Similarity
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13 ATGCATGAGAGAGGCCTCAGGCCAGGCAGAACCTCCAGAATGCTTTCATTGCTTTTTGT 72
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                                                          80.0%; Score 108; DB 20; ilarity 100.0%; Pred. No. 1.1e-26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 135; DB 20; 100.0%; Pred. No. 7.7e-36;
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                                                                                                  Length 108;
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Query Match
Best Local Similarity
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                                                                                              ; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9
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                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR TILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR APPLICATION NUMBER: 09912736.7
PRIOR APPLICATION NUMBER: 099549,872
PRIOR FILING DATE: 2000-04-14
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Publication No. US20040203027A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.2 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/10371101 Publication No. US20030149995A1 GENERAL INFORMATION:
                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 9
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PRIOR FILING DATE: 2002-12-02
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Pataret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035.US
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 108
TYPE: DNA
ORGANISM: mus musculus
                                                                                                                                                          ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
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                    Conservative
                                    37.6%;
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100.0%; Pred. No. 1.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                    Score 50.8; DB 1
Pred. No. 4.2e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                      Mismatches
                                                           DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                         Length
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                           Database :
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
 GenEmbl:*

1: gb_ba:*
2: gb_htg:
3: gb_in:
4: gb_ow
5: gb_ov
6: gb_p
7: gb_p
8: gb_p
10: gE
11: g'
11: g'
14:
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                           4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                                                                                                                                                                                     US-10-724-532-6
135
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                                                                                                                                                                                                                                                                                                                                                                        1 ctctctctcctcgagcagga.....tcatgcataagctttctctc 135
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                       9416466
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

ORIGIN	CDS	exon	mRNA	source	FEATURES	COMMENT	PUBMED	JOURNAL		TITLE	AUTHORS	REFERENCE	ORGANISM	SEGMENT	KEYWORDS	ACCESSION	DEFINITION	RESULT 1 RABPHLAM2/c
Tunction="regulatory protein of Barcopiasmic reticulum Ca-Affease" (codon_start=1 /product="phospholamban" /protein_id="AAA31445.1" /db_xref="GI:165639" /translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL ICTIVMLL"			<pre>/organism="oryctolagus cuniculus" /mol type="genomic DNA" /db_xref="taxon:9986" /tissue_lib="rabbit genomic" foin(M63600.1:855. 943.428858)</pre>	1858		Original source text: Rabbit DNA.	1828805	Chem. 266 (18),	d assignment of the gene to human chromosome 6	MacLennan, D.H. Structure of the rabbit phospholamban gene, cloning of the human	Fujii,J., Zarain-Herzberg,A., Willard,H.F., Tada,M. and	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. 1 (bases 1 to 858)	Oryctolagus cuniculus (Idopic)		phospholamban.	M63601	Rabbit phospholamban gene, partial exon 2.	

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RESULT 3
BD247907/c
LOCUS
                                                                                                          KEYWORDS
SOURCE
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AUTHORS
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KEYWORDS
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OCPHLAM/c
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MEDLINE
PUBMED
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 2841)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O.cuniculus mRNA for phospholamban.
Y00761
                                                                                                                              Method for screening composition for screeni
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                           de ens
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Mammalia; Eutheria;
1 (bases 1 to 159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phospholamban gene
FEBS Lett. 227 (1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phospholamban.
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                                                                                                                                                                                                                                                                                                                                                                                          AATAGGTTCTGGAGGTTTTGACGTGCTTGTTGAGGCATTTCA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAAGCATGACGATGATGCAGATCAGCAGGAGACATATCAAGATGAGACAGAAATTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAATCAGACAAAAAGCAATG
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nilarity 69.6%;
Conservative
                                                                                                                                                                                                                  for screening compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GOA:P20006"
/db_xref="UniProt/Swiss-Prot:P20006"
/translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL
ICIIVMLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="phospholamban"
/protein_id="CAA68730.1"
/db_xref="GI:1662"
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/mol_type="mRNA"
/db_xref="taxon:9986"
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Pred. No. 1.3e-05;
0; Mismatches 31;
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Pred. No. 1.1e-05;
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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VERSION
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Best Local S
Matches 70
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TITLE
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                                                                source
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                                                                                          Method for screening compounds

Patent: JP 2002541859-A 13 10-DEC-2002;

DEVGEN NV

OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PR 10-DEC-2000
PR 15-APR-1999 GB 9908670.4,15-APR-1999 US 61
PS 15-APR-1999 GB 9912736.7
PI RICHARD ZMAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42,C12N15/99,C12Q1/02,C12N15/00
CC Description of Artificial Sequence: HUMANIZED PIC Key
FT Source /organism='Artificial Sequence'.
FT Source /organism='Artificial Sequence'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEWGEN NV
OS Sus sp. (pig)
PN JP 200541859-A/9
PN 10-DEC-2002
PP 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4,15-APR-1999 US
OI-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL,JOSE GROENEN,THIERRY BOGAERT
PC C12Q1/42,C12N15/09,C12Q1/02,C12N15/00
CC Method for screening compounds
FH Key
1. 159
FT source
1. 159
FT source
1. 159
FT source
1. 159
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                                                                                                                                                                                                                                                                                                                                                                                                      synthetic construct
synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BD247911 159 bp Method for screening compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zwaal,R., Groenen,J. and Bogaert,T. Method for screening compounds Patent: JP 2002541859-A 9 10-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 159)
Zwaal, R., Groenen, J. and Bogaert, T.
                                                                                                                                                                                                                                                                                                                                                                                   other sequences; artificial sequences
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                                                                     /organism='Artificial
Location/Qualifiers
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            /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sus sp."
/mol_type="genomic DNA"
/db_xref="taxon:9826"
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Query Match
Best Local Similarity
Matches 70; Conser

Conservative

0;

Score 50.8; DB 6; Pred. No. 3.1e-05; D; Mismatches 32;

Length 159;

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37.6%;

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No.
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3117.004 Million cell updates/sec
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ABN22344
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ADP11384
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Aac64967 Pig phosp
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Aac06724 Human oRF
Aac06724 Human adu
Ab161825 Colon ade
Adn94087 Antipsori
Adp21384 Gene PLN
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Ach17005 Human adu
Ach18023 Human adu
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Ach18155 Human adu
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Ach26318 Human adu
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Ach30165 Human cDN
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Add99406 NOWel human pol
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ADQ21778 ADC66554 ADC66554 ACW43341 AAX24906 ADG79072 ABK74380 AAII1308 AAII1308 AAII1308 AAII13661 AAIA5661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661 AAIA661	AAC75801 AAC85836 AAL41031 ABG60653 ABG60653 ADP07907 ADC37617 ADC37617 ADC83658 ADF81658 ADF81658 ADF81658 ADF81658 ADF81658 ADF81658
Adq2177 Adc8655- Acn4434 Aax24906 Adq7907- Ab474380 Ab47307- Ab55007- Ab355007- Ab34661 Aba44562 Aba24770 Aak28730	Aac75801 Aa141031 Abq60653 Abq60653 Adg07907 Adl62294 Adc37611 Abk83658 Adf8141 Adr25391 Ac77530 Aac77586
Adq21778 Human sof Adc86554 Human GPC Acn4341 Mouse mRN Acx24906 Mouse elo Adq79072 Novel can Adq79072 Novel can Adx13308 Probe #32 Aba55007 Human foe Aai14661 Probe #33 Aba44667 Probe #33 Aba44770 Probe #33 Aba44770 Probe #32	503797271
8 Human sof 4 Human sof 1 Mouse mRN Mouse elo Novel can Bacillus Probe #32 Human foe Probe #33 Human bre Probe #32 Human bre Probe #32	Human ORF Nuclectid DNA encod Human col 7 Human nuc Human nuc Luman cDN 2 Leukaemia 9 Breast ca 9 Ureukaemia 9 Tumour-as Human ova Human ova

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RESULT 1
AAC64967/c
D AAC64967 standard;
15-APR-1999;
15-APR-1999;
01-JUN-1999;
                                                                                                                                                                                                  Pig; sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling; cardiac hypertrophy; heart failure; hypertension; Darier-White disease; Brodys disease; diabetes; ss.
                                                                                                                                                                                       Sus scrofa.
                                                                                                                                                                                                                              Pig phospholamban
                                                                                                                                                                                                                                            09-FEB-2001
                                                                                                                                               14-APR-2000; 2000GB-00009363.
                                                                                                                                                            25-OCT-2000
                                                                                                                                                                                                                                                        AAC64967;
                                                                                                        (DEVG-) DEVGEN
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99US-0129596P.
99GB-00012736.
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                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                      ВP
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The present invention is concerned with methods of using C. elegans identify compounds which are capable of up- and down-regulating the activity of the sacro/endoplasmic reticulum calcium ATPase (SERCA). protein is involved in cell signalling, and elevated levels affect cellular processes such as contraction, secretion and cell cycling.

This The

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Identifying modulators of sarco/endoplasmic reticulum calcium ATPouseful potentially for treating disorders of calcium homeostasis, cardiac hypertrophy.

e.9

Disclosure; Fig 11; 108pp; English.

WPI; Zwaal

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Groenen J,

Bogaert

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2000-658082/64.

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RESULT 2
ADB53082/c
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11-APR-2002
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19-APR-2002
22-APR-2002
08-MAY-2002
09-MAY-2002
09-MAY-2002
09-MAY-2002
                                                              Mendrick
Elashoff
                                                                                                                                                                                                                                                                                                                                                                                        toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene expressiprofile of a tissue or cell sample to a database of Tox mean and non-T
                                          WPI;
                                                                                                                                    09-JUL-2002;
                                                                                                                                                                                                                                                         08-APR-2002;
10-APR-2002;
                                                                                                                                                                                                                                                                              04-FEB-2002;
13-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus.
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                                          2003-731472/69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be used to identify compounds for use in the treatment
                                                                                                                                                     2002US-0370248P.
2002US-0371134P.
2002US-0371135P.
2002US-0371150P.
2002US-0373413P.
2002US-0373602P.
2002US-0374139P.
2002US-0378652P.
2002US-0378655P.
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                                                                                            LOGIC
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2002US-0363534P.
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2003US-0442900P.
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2002US-0394253P.
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                                                                        Porter M,
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Pred. No. 6.
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  comprises comparing a gene expression to a database of Tox mean and non-Tox
                                                                      Higgs
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                                                                                                       The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for
Sequence
                                                        drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
     701
  B₽;
     184
  A; 178 C;
  141 G; 198 T; 0 U; 0 Other;
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                                          329
                                                                16
                    76
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                                                                                              Similarity
             GAAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA 118
                                          CAGAAGCATCACAATGATGCATATCAGCAGCAGACATATCAAGATGAGACAGAAATTGAT 270
                                                              CAGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAATCAGACAAAAAGCAAT
AAAGAGGTTCTGGAGGTTCTGACGCGCTTGCTGGGGGCATTTCA
                                                                                     Conservative
                                                                                             37.2%;
                                                                                     0,
                                                                                                Score 50.2;
Pred. No. 1
                                                                                     Mismatches
                                                                                                1.7e-05
                                                                                                          DB 10;
                                                                                      33;
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                                                                                                           Length
 227
                                                                                                           701;
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269

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RESULT 3
ADR97285/c
                                                                                               US2004191802-A1
                                                                                                                                                                                           Human phospholamban polymorphism fragment
                                                                                                                                                                                                                                                            ADR97285;
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22-OCT-2002;
                               22-OCT-2003; 2003US-00691412
                                                               30-SEP-2004
                                                                                                                                                                                                                            16-DEC-2004
                                                                                                                                                           human; phospholamban; polymorphism; cardiovascular disease.
                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                        standard; DNA; 159
 2002US-0420295P
                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                DNA.
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The invention relates to a method of phospholamban polymorphism assessment in an individual which comprises comparing the analysis nucleotide fragment with a predetermined phospholamban nucleotide fragment sequence to determine whether the individual carries a phospholamban polymorphism. The methods and phospholamban polymorph fragment are useful for determining if an individual is at risk for Phospholamban polymorphism assessment in individual, for determining for developing cardiovascular disease, by comparing analysis of the nucleotide fragment with a predetermined phospholamban nucleotide Claim 15; SEQ ID NO 1; 15pp; English riek the

polymorphism ; risk for

WPI; 2004-689841/67

Kranias

EG,

Haghighi

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(HAGH/) (KRAN/)

KRANIAS E G. HAGHIGHI K.

Claim 44; SEQ ID

NO 3624; 874pp; English

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REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS ORIGIN RESULT 1 BX669692/c FEATURES DEFINITION TITLE Bource Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this Chemin de Borde-Rouge - Au cedex, FRANCE Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08 Contact: Tosser-Klopp G Genetique Animale Institut National de la Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (Dases 1 to 381)

Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S., Soares, M., Bonaldo, F. and Hatey, F. Sus scrofa (pig) Sus scrofa BX669692 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0028i.c.02 Sprim, mRNA sequence. A Pig Normalised Multi-Tissue CDNA Library Unpublished (2003) BX669692 BX669692.1 GI:37979481 0028 row: c /clone="scac00281.c.02"
/tissue_type="mixed"
/clone_Tib="Sus Scrofa library (scac)"
/clone_Tib="Sus Scrofa library (scac)"
/clone_Tib="Sus Scrofa library tissues: adipose tissue,
/note="Vector: p773D-pac vector; tissues: heart,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo uretral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder" /organism="Sus scrofa" /mol_type="mRNA" /db_xref="taxon:9823" ocation/Qualifiers column: 2. Recherche Auzeville Agronomique BP27, 31326 Castanet-Tolosan EST 07-MAY-2004

Query Match

37.6%;

Score 50.8;

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Euteleostomi;

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Soares,M., Bonaldo,F. and Hatey,F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
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1 (bases 1 to 702)
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Location/Qualifiers
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/tissue_type="mixed"
/dev_stage="from embryos to adults"
/dev_stage="from embryos to sadults"
/clone_lib="Sus Scrofa library (scan)"
/clone_lib-"Sus Scrofa library (scan)"
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/mol_type="mRNA"
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Pred. No. 0.00033;
0; Mismatches 32;
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Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonnet,A., Tosser-Klopp,G., Benne,F., Caban
Soares,M., Bonaldo,F. and Hatey,F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
Contact: Tosser-Klopp G
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Sus scrofa
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BX674983
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                   1 (bases 1 to 740)
Bonnet, A., Tosser-K
                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                   Sus scrofa
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 724)
  Soares, M.,
                                                                                                                                                         Sus scrofa (pig)
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/clone="scac0039i.h.23"
/clone="scac0039i.h.23"
/tissue_type="mixed"
/clone_Tib="Sus Scrofa library (scac)"
/clone="Vector: pT773D-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"
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Tosser-Klopp,G., Benne,
Bonaldo,F. and Hatey,F.
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                        Benne, F.,
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Result
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Listing first 45 summaries
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  50.8
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-312-283C-203
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                   Sequence 13, Appl Sequence 10799, A Sequence 10799, A Sequence 13181, A Sequence 26, Appl Sequence 1076, Appl Sequence 1076, Appl Sequence 1172, Appl Sequence 1172, Appl Sequence 1172, Appl Sequence 1536, A Sequence 1536, Appl Sequence 1562, Appl Sequence 1704, Appl Sequence 1704, Appl Sequence 1701, Appl Sequence 1701, Appl Sequence 2020, Appl Sequence 2030, Appl Sequence 203, Appl Sequence 28, App
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US-09-549-872B-9/c
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Sequence 160, App Sequence 1, Appli			Sequence 1, Appli Sequence 1929, Ap	Sequence 17390, A Sequence 17391, A Sequence 1, Appli	Sequence 16824, A Sequence 12086, A	Sequence 5041, Ap Sequence 200644, Sequence 200790,

ALIGNMENTS

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; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9
                                                                                                                                          RESULT 2
US-09-549-872B-13/c
US-09-549-872B-13/c
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; Patent INFORMATION:
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APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: BOGAERT, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR APPLICATION NUMBER: GB 908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 9
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Best Local Similarity 68.6
Matches 70; Conservative
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APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
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Pred. No. 1.2e-07;
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Patent No. 6783961

FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO. 10799
                     RESULT 4
US-09-949-016-1439/c
US-09-949-016-1439/ Application US/09949016
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; Patent No. 6812339
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PRIOR FILING DATE: 1999-04-15
PRIOR PELICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
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LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
BENERAL INFORMATION:
APPLICANT: VENTER, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Descript
OTHER INFORMATION: PLB cDNA
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                Match 34.1%;
Local Similarity 65.7%;
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Local Similarity 68.6%;
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                                                                                                                                                   AATAGATTCTGTAGCTTTTGACGTGCTTGTTGAGGCATTTCA 249
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 Craig et al
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Pred. No. 8.4e-
0; Mismatches
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Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                               8.4e-06;
ches 35;
                                                                                                                                                                                                                                                                                                                                     DB 4; Length 480;
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; ORGANISM: Human
US-09-949-016-1439
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TITLE OF INVENTION: POLYMORPHISMS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
PRIOR FILLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13181
LENGTH: 16062
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Best Local Similarity
Matches 67; Conserv
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                         Local Similarity nes 67; Conserv
12702
                                                                                        12762
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                                         AAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA 118
AATAGATTCTGTAGCTTTTGACGTGCTTGTTGAGGCATTTCA
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Pred. No. 4.2e-05;
0; Mismatches 35;
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Pred. No. 1.5e-05;
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OF DETECTION
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RESULT 6
US-09-124-671-26/c
; Sequence 26, Application US/09124671A

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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135
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/cgn2_6/ptodata/1/pubpna/US07_FUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW FUB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB. Beq:*
/cgn2 6/ptodata/1/pubpna/PCT NEW PUB. Beq:*
/cgn2 6/ptodata/1/pubpna/US06 NEW PUB. Beq:*
/cgn2 6/ptodata/1/pubpna/US05 PUBCOMB. Beq:*
/cgn2 6/ptodata/1/pubpna/US07 NEW PUB. Beq:*
                                                                                                                                            [6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
[6/ptodata/1/pubpna/US11_R_PUBCOMB.seq:*
[6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
[6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
[6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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SUMMARIES
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2603.465 Million cell updates/sec
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46	50.8	50.8	108	108	135	135	Score
34.1	37.6	37.6	80.0	80.0	100.0	100.0	Query Match 1
159	159	159	108	108	135		Query Match Length DB
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US-10-691-412-1	US-10-371-101-13	US-10-371-101-9	US-10-724-532-4	US-10-724-532-3	US-10-724-532-6	US-10-724-532-5	DB ID
Ļ	Sequence 13, Appl	Sequence 9, Appli	4	Sequence 3, Appli	Sequence 6, Appli		Description

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22.7		•	22.8	•	•	•	•	•	•	•	•	•	•	•	•	24.9	•	•	•	. 6			·o	•	25.9	•	•	•	•	•	•	32.9	•	•	•	•	34.1
1878	1591	639	415							3306						2419						10625			6481	492	407	315	315	315	487	394	418	380	1635		525
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US-10-369-493-43089	US-10-437-963-78016	US-10-470-048B-40	US-09-864-761-3236	US-09-974-300-1671	US-10-437-963-88641	US-09-832-292-7	US-09-994-485-3	US-10-087-192-740	US-10-767-701-25701	US-10-292-798-1007	US-10-723-860-4598	US-09-925-301-80	US-10-848-755A-148	342	-10-	-09-814-353-	-0-	-10-425-114-	US-10-723-518-2	US-09-969-034-4348	US-10-690-276-3	US-10-023-219-3	09-7	-10	US-10-037-270-1076	-09	-09	-10-873-594	-10-877-930	-10-815	-09-918	-09-918-995-	-09-918	-09-918-995-395	-10-843-641	US-09-873-367C-162	US-09-918-995-4045
Sequence 43089, A	7801		3236,	Sequence 1671, Ap				Sequence 740, App		1007,	45	80, Ar	148,	1260,	1260,	20506,	1677	557		٤		۳	5	1076,		e 17377	384:		e 26,	e 26,	537	4217,	5235,	Sequence 3950, Ap	162,		045,

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CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 135
TYPE: DNA
ORGANISM: mus musculus
US-10-724-532-5
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US-10-724-532-5/c
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Publication No. US20040203027A1
GENERAL INFORMATION:
                                                                                                                              Query Match 100.0%; Score 135; DB 20; Best Local Similarity 100.0%; Pred. No. 7.7e-36; Matches 135; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo) plasmic TITLE OF INVENTION: Reticulum FILE REFERENCE: SR RPA
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                                            135 CTCTCTCTCGAGCAGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAAT
  61 CAGACAAAAAGCAATGAAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCATG 120
                                                                    1 CTCTCTCCTCGAGCAGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAAT 60
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; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6
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CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10724532 Publication No. US20040203027A1 GENERAL INFORMATION:
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APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
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Publication No. US20040203027A1
                                                           Matches
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                 SEQ ID NO 3
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Best Local (
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CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOPTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
                                                                                                                                                     LENGTH: 108
TYPE: DNA
ORGANISM: mus musculus
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                                                           108;
16 CAGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAATCAGACAAAAAGCAAT
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                                                                                                 Length 108;
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                                                             Indels
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Query Match
Best Local Similarity
Thes 70; Conserva
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CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: 09912736.7
PRIOR PILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR APPLICATION NUMBER: 09/549,872
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CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10724532 Publication No. US20040203027A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/10371101 Publication No. US20030149995A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
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TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
                                                                                                                LENGTH: 159
TYPE: DNA
ORGANISM: Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590,70035.US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 108
TYPE: DNA
ORGANISM: mus musculus
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              37.6%; ilarity 68.6%; Conservative
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100.0%; Pred. No. 1.1e-26;
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                                  Score 50.8; DB 1
Pred. No. 4.2e-07
                     Mismatches
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                                                         DB 15;
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                                                         Length 159;
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